



FIGURE 10

Figure 10. Oligonucleotide Primers for QuikChange Mutagenesis

V93E#1

5'-gAACATCCCCAAGATgAACCCACTATTAgAgAAAAAg-3' (SEQ ID NO: 5)

V93E#2

5'-CTTTTCTCTAATAgTgggTTCATCTTggggATgTTC-3' (SEQ ID NO: 6)

V93R#1

5'-gAACATCCCCAAGATAgACCCACTATTAgAgAAAAAg-3' (SEQ ID NO: 7)

V93R#2

5'-CTTTTCTCTAATAgTgggTCTATCTTggggATgTTC-3' (SEQ ID NO: 8)

V93N#1

5'-gAACATCCCCAAGATAACCCCACTATTAgAgAAAAAg-3' (SEQ ID NO: 9)

V93N#2

5'-CTTTTCTCTAATAgTggggTTATCTTggggATgTTC-3' (SEQ ID NO: 10)

V93H#1

5'-gAACATCCCCAAGATCACCCCACTATTAgAgAAAAAg-3' (SEQ ID NO: 11)

V93H#2

5'-CTTTTCTCTAATAgTggggTgATCTTggggATgTTC-3' (SEQ ID NO: 12)

V93X (for saturation mutagenesis; obtained V93G and V93L mutants from library)

5'-(Phosphate)gAACATCCCCAAGATNNKCCCACTATTAgAgAAAAAg-3' (SEQ ID NO: 13)

Replacement Figure

V93K#1

5'-gAACATCCCCAAGATAAACCCCTATTAgAg-3' (SEQ ID NO: 14)

V93K#2

5'-CTCTAATAgTgggTTTATCTTggggATgTTC-3' (SEQ ID NO: 15)

QCM#1 5'-(Phosphate)gAACATCCCCAAGATgCCCCCACTATTAgAgAAAAAg-(SEQ ID NO: 16)'

Alanine

QCM#2 5'-(Phosphate)gAACATCCCCAAGATgACCCCCTATTAgAgAAAAAg-3'(SEQ ID NO: 17)

Aspartic Acid

QCM#3 5'-(Phosphate)gAACATCCCCAAGATTgCCCCCTATTAgAgAAAAAg-3' (SEQ ID NO: 18)

Cysteine

QCM#4 5'-(Phosphate)gAACATCCCCAAGATATACCCCCTATTAgAgAAAAAg-3' (SEQ ID NO: 19)

Isoleucine

QCM#5 5'-(Phosphate)gAACATCCCCAAGATATgCCCCTATTAgAgAAAAAg-3' (SEQ ID NO: 20)

Methionine

QCM#6 5'-(Phosphate)gAACATCCCCAAGATTTCCCCCTATTAgAgAAAAAg-3' (SEQ ID NO: 21)

Replacement Figure

Phenylalanine

QCM#7 5'-(Phosphate)gAACATCCCCAAGATCCTCCCCTATTAgAgAAAAAg-3' (SEQ ID NO: 22)

Proline

QCM#8 5'-(Phosphate)gAACATCCCCAAGATAgCCCCCTATTAgAgAAAAAg-3' (SEQ ID NO: 23)

Serine

QCM#9 5'-(Phosphate)gAACATCCCCAAGATACCCCCTATTAgAgAAAAAg- 3' (SEQ ID NO: 24)

Threonine

QCM#10 5'-(Phosphate)gAACATCCCCAAGATTACCCCCTATTAgAgAAAAAg-3' (SEQ ID NO: 25)

Tyrosine

QCM#11 5'-(Phosphate)gAACATCCCCAAGATTggCCCCTATTAgAgAAAAAg-3'

(SEQ ID NO: 26)

Tryptophan

Replacement Figure

FIGURE 13A**PFU DNA POLYMERASE**

V93R MUTANT: NNN = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) (SEQ ID NO: 27)

V93E MUTANT: NNN = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) (SEQ ID NO: 28)

```
ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATNNNC CCACTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420
GATATAGAAA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTTCC ATATTTAGCG 660
AAAAGGGCAG AAAAAGTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
GAACTCGGGA AAGAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140
CTCAGGGAGA GCTACACAGG TGGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGAAGAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAAATTGCA 1860
AAAGAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCTTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCCTAG 2328
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PFU DNA POLYMERASE

G387P Mutant (CCN is the codon for Proline where N = C, G, A, or T)

V93R MUTANT: NNN = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) (SEQ ID NO: 29)

V93E MUTANT: NNN = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) (SEQ ID NO: 30)

```
ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATNNNC CCACTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420
GATATAGAAA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTTCC ATATTTAGCG 660
AAAAGGGCAG AAAAACTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
GAACTCGGGA AAGAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140
CTCAGGGAGA GCTACACACC NGGATTTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCTG GGAAGAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAAATTGCA 1860
AAAGAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040
GTAGCTGTTG CAAAGAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCCTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCCTAG 2328
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PFU DNA POLYMERASE

D141A/E143A Mutant (GCN is the codon for alanine where N = C, G, A, or T)

V93R MUTANT: NNN = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) (SEQ ID NO: 31)

V93E MUTANT: NNN = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) (SEQ ID NO: 32)

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ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
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CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATNNNC CCACTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTCG AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420
GCNATAGCNA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTTCC ATATTTAGCG 660
AAAAGGGCAG AAAAAGCTTG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
GAACTCGGGA AAGAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140
CTCAGGGAGA GCTACACAGGTGGATTCTGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGGAAGAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAAATTGCA 1860
AAAGAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040
GTAGCTGTTG CAAAGAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCCTTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTGGA TACAGAAAGG AAGACCTCAG ATACCAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCCTAG 2328

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KOD DNA POLYMERASE

V93R MUTANT: NNN = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) (SEQ ID NO: 33)

V93E MUTANT: NNN = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) (SEQ ID NO: 34)

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ATGATCCTCG ACACTGACTA CATAACCGAG GATGGAAAGC CTGTCATAAG AATTTTCAAG 60
AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT TTGAACCTTA CTTCTACGCC 120
CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAAGA TAACCGCCGA GAGGCACGGG 180
ACGGTTGTAA CGGTTAAGCG GGTGAAAAG GTTCAGAAGA AGTTCCTCGG GAGACCAGTT 240
GAGGTCTGGA AACTCTACTT TACTCATCCG CAGGACNNNC CAGCGATAAG GGACAAGATA 300
CGAGAGCATC CAGCAGTTAT TGACATCTAC GAGTACGACA TACCCTTCGC CAAGCGCTAC 360
CTCATAGACA AGGGATTAGT GCCAATGGAA GGCGACGAGG AGCTGAAAAT GCTCGCCTTC 420
GACATTGAAA CTCTCTACCA TGAGGGCGAG GAGTTCGCCG AGGGGCCAAT CCTTATGATA 480
AGCTACGCCG ACGAGGAAGG GGCCAGGGTG ATAAGTTGGA AGAACGTGGA TCTCCCCTAC 540
GTTGACGTCG TCTCGACGGA GAGGGAGATG ATAAAGCGCT TCCTCCGTGT TGTGAAGGAG 600
AAAGACCCGG ACGTTCTCAT AACCTACAAC GGCGACAAC TCGACTTCGC CTATCTGAAA 660
AAGCGCTGTG AAAAGCTCGG AATAAACTTC GCCCTCGGAA GGGATGGAAG CGAGCCGAAG 720
ATTCAGAGGA TGGGCGACAG GTTTGCCGTC GAAGTGAAGG GACGGATACA CTTCGATCTC 780

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TATCCTGTGA	TAAGACGGAC	GATAAACCTG	CCCACATACA	CGCTTGAGGC	CGTTTATGAA	840
GCCGTCCTCG	GTCAGCCGAA	GGAGAAGGTT	TACGCTGAGG	AAATAACCAC	AGCCTGGGAA	900
ACCGGCGAGA	ACCTTGAGAG	AGTCGCCCCG	TACTCGATGG	AAGATGCGAA	GGTCACATAC	960
GAGCTTGGGA	AGGAGTTCCT	TCCGATGGAG	GCCCAGCTTT	CTCGCTTAAT	CGGCCAGTCC	1020
CTCTGGGACG	TCTCCCGCTC	CAGCACTGGC	AACCTCGTTG	AGTGGTTCCT	CCTCAGGAAG	1080
GCCTATGAGA	GGAATGAGCT	GGCCCCGAAC	AAGCCCGATG	AAAAGGAGCT	GGCCAGAAGA	1140
CGGCAGAGCT	ATGAAGGAGG	CTATGTAAAA	GAGCCCGAGA	GAGGGTTGTG	GGAGAACATA	1200
GTGTACCTAG	ATTTTAGATC	CCTGTACCCC	TCAATCATCA	TCACCCACAA	CGTCTCGCCG	1260
GATACGCTCA	ACAGAGAAGG	ATGCAAGGAA	TATGACGTTG	CCCCACAGGT	CGGCCACCGC	1320
TTCTGCAAGG	ACTTCCCAGG	ATTTATCCCG	AGCCTGCTTG	GAGACCTCCT	AGAGGAGAGG	1380
CAGAAGATAA	AGAAGAAGAT	GAAGGCCACG	ATTGACCCGA	TCGAGAGGAA	GCTCCTCGAT	1440
TACAGGCAGA	GGGCCATCAA	GATCCTGGCA	AACAGCTACT	ACGGTTACTA	CGGCTATGCA	1500
AGGGCGCGCT	GGTACTGCAA	GGAGTGTGCA	GAGAGCGTAA	CGGCCTGGGG	AAGGGAGTAC	1560
ATAACGATGA	CCATCAAGGA	GATAGAGGAA	AAGTACGGCT	TTAAGGTAAT	CTACAGCGAC	1620
ACCGACGGAT	TTTTTGCCAC	AATACCTGGA	GCCGATGCTG	AAACCGTCAA	AAAGAAGGCT	1680
ATGGAGTTCC	TCAAGTATAT	CAACGCCAAA	CTTCCGGGCG	CGCTTGAGCT	CGAGTACGAG	1740
GGCTTCTACA	AACGCGGCTT	CTTCGTCACG	AAGAAGAAGT	ATGCGGTGAT	AGACGAGGAA	1800
GGCAAGATAA	CAACGCGCGG	ACTTGAGATT	GTGAGGCGTG	ACTGGAGCGA	GATAGCGAAA	1860
GAGACGCAGG	CGAGGGTTCT	TGAAGCTTTG	CTAAAGGACG	GTGACGTCGA	GAAGGCCGTG	1920
AGGATAGTCA	AAGAAGTTAC	CGAAAAGCTG	AGCAAGTACG	AGGTTCCGCC	GGAGAAGCTG	1980
GTGATCCACG	AGCAGATAAC	GAGGGATTTA	AAGGACTACA	AGGCAACCGG	TCCCCACGTT	2040
GCCGTTGCCA	AGAGGTGCGC	CGCGAGAGGA	GTCAAAATAC	GCCCTGGAAC	GGTGATAAGC	2100
TACATCGTGC	TCAAGGGCTC	TGGGAGGATA	GGCGACAGGG	CGATACCGTT	CGACGAGTTC	2160
GACCCGACGA	AGCACAAGTA	CGACGCCGAG	TACTACATTG	AGAACCAGGT	TCTCCCAGCC	2220
GTTGAGAGAA	TTCTGAGAGC	CTTCGGTTAC	CGCAAGGAAG	ACCTGCGCTA	CCAGAAGACG	2280
AGACAGGTTG	GTTTGAGTGC	TTGGCTGAAG	CCGAAGGGAA	CTTGA	2325	

Vent DNA POLYMERASE

V93R MUTANT: NNN = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) (SEQ ID NO: 35)

V93E MUTANT: NNN = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) (SEQ ID NO: 36)

ATGATACTGG	ACACTGATTA	CATAACAAAA	GATGGCAAGC	CTATAATCCG	AATTTTAAAG	60
AAAGAGAACG	GGGAGTTTAA	AATAGAACTT	GACCCTCATT	TTCAGCCCTA	TATATATGCT	120
CTTCTCAAAG	ATGACTCCGC	TATTGAGGAG	ATAAAGGCAA	TAAAGGGCGA	GAGACATGGA	180
AAAACGTGTA	GAGTGCTCGA	TGCAGTGAAA	GTCAGGAAAA	AATTTTGGG	AAGGGAAGTT	240
GAAGTCTGGA	AGCTCATTTT	CGAGCATCCC	CAAGACNNNC	CAGCTATGCG	GGGCAAAATA	300
AGGGAACATC	CAGCTGTGGT	TGACATTTAC	GAATATGACA	TACCCTTTGC	CAAGCGTTAT	360
CTCATAGACA	AGGGCTTGAT	TCCCATGGAG	GGAGACGAGG	AGCTTAAGCT	CCTTGCCTTT	420
GATATTGAAA	CGTTTTATCA	TGAGGGAGAT	GAATTTGGAA	AGGGCGAGAT	AATAATGATT	480
AGTTATGCCG	ATGAAGAAGA	GGCCAGAGTA	ATCACATGGA	AAAATATCGA	TTTGCCGTAT	540
GTCGATGTTG	TGTCCAATGA	AAGAGAAATG	ATAAAGCGTT	TTGTTCAAGT	TGTTAAAGAA	600
AAAGACCCCG	ATGTGATAAT	AACTTACAAT	GGGGACAATT	TTGATTTGCC	GTATCTCATA	660
AAACGGGCAG	AAAAGCTGGG	AGTTCGGCTT	GTCTTAGGAA	GGGACAAAGA	ACATCCCGAA	720
CCCAAGATTC	AGAGGATGGG	TGATAGTTTT	GCTGTGGAAA	TCAAGGGTAG	AATCCACTTT	780
GATCTTTTCC	CAGTTGTGCG	AAGGACGATA	AACCTCCCAA	CGTATACGCT	TGAGGCAGTT	840
TATGAAGCAG	TTTTAGGAAA	AACCAAAAGC	AAATTAGGAG	CAGAGGAAAT	TGCCGCTATA	900
TGGGAAACAG	AAGAAAGCAT	GAAAAAATA	GCCCAGTACT	CAATGGAAGA	TGCTAGGGCA	960
ACGTATGAGC	TCGGGAAGGA	ATTCTTCCCC	ATGGAAGCTG	AGCTGGCAAA	GCTGATAGGT	1020
CAAAGTGTAT	GGGACGTCTC	GAGATCAAGC	ACCGGCAACC	TCGTGGAGTG	GTATCTTTTA	1080
AGGGTGGCAT	ACGCGAGGAA	TGAAC TTGCA	CCGAACAAAC	CTGATGAGGA	AGAGTATAAA	1140
CGGCGCTTAA	GAACAACTTA	CCTGGGAGGA	TATGTAAAAG	AGCCAGAAAA	AGGTTTGTGG	1200
GAAAATATCA	TTTATTTGGA	TTTCCGCAGT	CTGTACCCTT	CAATAATAGT	TACTCACAAAC	1260
GTATCCCCAG	ATACCCTTGA	AAAAGAGGGC	TGTAAGAATT	ACGATGTTGC	TCCGATAGTA	1320
GGATATAGGT	TCTGCAAGGA	CTTTCCGGGC	TTTATTCCCT	CCATACTCGG	GGACTTAATT	1380
GCAATGAGGC	AAGATATAAA	GAAGAAAATG	AAATCCACAA	TTGACCCGAT	CGAAAAGAAA	1440
ATGCTCGATT	ATAGGCAAAG	GGCTATTAAA	TTGCTTGCAA	ACAGCTATTA	CGGCTATATG	1500

GGGTATCCTA	AGGCAAGATG	GTACTCGAAG	GAATGTGCTG	AAAGCGTTAC	CGCATGGGGG	1560
AGACACTACA	TAGAGATGAC	GATAAGAGAA	ATAGAGGAAA	AGTTCGGCTT	TAAGGTTCTT	1620
TATGCGGACA	CTGACGGCTT	TTATGCCACA	ATACCCGGGG	AAAAGCCTGA	ACTCATTAAG	1680
AAGAAAGCCA	AGGAATTCCT	AAACTACATA	AACTCCAAAC	TTCCAGGTCT	GCTTGAGCTT	1740
GAGTATGAGG	GCTTTTACTT	GAGAGGATTC	TTTGTTACAA	AAAAGCGCTA	TGCAGTCATA	1800
GATGAAGAGG	GCAGGATAAC	AACAAGGGGC	TTGGAAGTAG	TAAGGAGAGA	TTGGAGTGAG	1860
ATAGCTAAGG	AGACTCAGGC	AAAGGTTTTA	GAGGCTATAC	TTAAAGAGGG	AAGTGTTGAA	1920
AAAGCTGTAG	AAGTTGTTAG	AGATGTTGTA	GAGAAAATAG	CAAAATACAG	GGTTCCTACT	1980
GAAAAGCTTG	TTATCCATGA	GCAGATTACC	AGGGATTTAA	AGGACTACAA	AGCCATTGGC	2040
CCTCATGTCT	CGATAGCAAA	AAGACTTGCC	GCAAGAGGGA	TAAAAGTGAA	ACCGGGCACA	2100
ATAATAAGCT	ATATCGTTCT	CAAAGGGAGC	GGAAAGATAA	GCGATAGGGT	AATTTTACTT	2160
ACAGAATACG	ATCCTAGAAA	ACACAAGTAC	GATCCGGACT	ACTACATAGA	AAACCAAGTT	2220
TTGCCGGCAG	TACTTAGGAT	ACTCGAAGCG	TTTGATACAA	GAAAGGAGGA	TTTAAGGTAT	2280
CAAAGCTCAA	AACAAACCGG	CTTAGATGCA	TGGCTCAAGA	GGTAG		2325

Deep Vent

V93R MUTANT: NNN = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) (SEQ ID NO: 37)

V93E MUTANT: NNN = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) (SEQ ID NO: 38)

ATGATACTTG	ACGCTGACTA	CATCACCAG	GATGGGAAGC	CGATTATAAG	GATTTTCAAG	60
AAAGAAAACG	GCGAGTTTAA	GGTTGAGTAC	GACAGAAACT	TTAGACCTTA	CATTTACGCT	120
CTCCTCAAAG	ATGACTCGCA	GATTGATGAG	GTTAGGAAGA	TAACCGCCGA	GAGGCATGGG	180
AAGATAGTGA	GAATTATAGA	TGCCGAAAAG	GTAAGGAAGA	AGTTCCTGGG	GAGGCCGATT	240
GAGGTATGGA	GGCTGTACTT	TGAACACCCT	CAGGACNNNC	CCGCAATAAG	GGATAAGATA	300
AGAGAGCATT	CCGCAGTTAT	TGACATCTTT	GAGTACGACA	TTCCGTTTCG	GAAGAGGTAC	360
CTAATAGACA	AAGGCCTAAT	TCCAATGGAA	GGCGATGAAG	AGCTCAAGTT	GCTCGCATTT	420
GACATAGAAA	CCCTCTATCA	CGAAGGGGAG	GAGTTCGCGA	AGGGGCCCAT	TATAATGATA	480
AGCTATGCTG	ATGAGGAAGA	AGCCAAAGTC	ATAACGTGGA	AAAAGATCGA	TCTCCCGTAC	540
GTCGAGGTAG	TTTCCAGCGA	GAGGGAGATG	ATAAAGCGGT	TCCTCAAGGT	GATAAGGGAG	600
AAAGATCCCG	ATGTTATAAT	TACCTACAAC	GGCGATTCTT	TCGACCTTCC	CTATCTAGTT	660
AAGAGGGCCG	AAAAGCTCGG	GATAAAGCTA	CCCCTGGGAA	GGGACGGTAG	TGAGCCAAAG	720
ATGCAGAGGC	TTGGGGATAT	GACAGCGGTG	GAGATAAAGG	GAAGGATACA	CTTTGACCTC	780
TACCACGTGA	TTAGGAGAAC	GATAAACCTC	CCAACATACA	CCCTCGAGGC	AGTTTATGAG	840
GCAATCTTCG	GAAAGCCAAA	GGAGAAAGTT	TACGCTCACG	AGATAGCTGA	GGCCTGGGAG	900
ACTGGAAAGG	GACTGGAGAG	AGTTGCAAAG	TATTCAATGG	AGGATGCAAA	GGTAACGTAC	960
GAGCTCGGTA	GGGAGTTCTT	CCCAATGGAG	GCCCAGCTTT	CAAGGTTAGT	CGGCCAGCCC	1020
CTGTGGGATG	TTTCTAGGTC	TTCAACTGGC	AACTTGGTGG	AGTGGTACCT	CCTCAGGAAG	1080
GCCTACGAGA	GGAATGAATT	GGCTCCAAAC	AAGCCGGATG	AGAGGGAGTA	CGAGAGAAGG	1140
CTAAGGGAGA	GCTACGCTGG	GGGATACGTT	AAGGAGCCGG	AGAAAGGGCT	CTGGGAGGGG	1200
TTAGTTTCCC	TAGATTTTCAG	GAGCCTGTAC	CCCTCGATAA	TAATCACCCA	TAACGTCTCA	1260
CCGGATACGC	TGAACAGGGA	AGGGTGTAGG	GAATACGATG	TCGCCCCAGA	GGTTGGGCAC	1320
AAGTTCTGCA	AGGACTTCCC	GGGGTTTATC	CCCAGCCTGC	TCAAGAGGTT	ATTGGATGAA	1380
AGGCAAGAAA	TAAAAAGGAA	GATGAAAGCT	TCTAAAGACC	CAATCGAGAA	GAAGATGCTT	1440
GATTACAGGC	AACGGGCAAT	CAAAATCCTG	GCAAACAGCT	ATTATGGGTA	TTATGGGTAC	1500
GCAAAAGCCC	GTTGGTACTG	TAAGGAGTGC	GCAGAGAGCG	TTACGGCCTG	GGGGAGGGAA	1560
TATATAGAGT	TCGTAAGGAA	GGAAGTGGAG	GAAAAGTTTC	GGTTCAAAGT	CTTATACATA	1620
GACACAGATG	GACTCTACGC	CACAATTCCT	GGGGCAAAAC	CCGAGGAGAT	AAAGAAGAAA	1680
GCCCTAGAGT	TCGTAGATTA	TATAAACGCC	AAGCTCCCAG	GGCTGTTGGA	GCTTGAGTAC	1740
GAGGGCTTCT	ACGTGAGAGG	GTTCTTCGTG	ACGAAGAAGA	AGTATGCGTT	GATAGATGAG	1800
GAAGGGAAGA	TAATCACTAG	GGGGCTTGAA	ATAGTCAGGA	GGGACTGGAG	CGAAATAGCC	1860
AAAGAAACCC	AAGCAAAAGT	CCTAGAGGCT	ATCCTAAAGC	ATGGCAACGT	TGAGGAGGCA	1920
GTAAAGATAG	TTAAGGAGGT	AACTGAAAAG	CTGAGCAAGT	ACGAAATACC	TCCAGAAAAG	1980
CTAGTTATTT	ACGAGCAGAT	CACGAGGCC	CTTCACGAGT	ACAAGGCTAT	AGGTCCGCAC	2040
GTTGCCGTGG	CAAAAAGGTT	AGCCGCTAGA	GGAGTAAAGG	TGAGGCCTGG	CATGGTGATA	2100
GGGTACATAG	TGCTGAGGGG	AGACGGGCCA	ATAAGCAAGA	GGGCTATCCT	TGCAGAGGAG	2160
TTGATCTCA	GGAAGCATAA	GTATGACGCT	GAGTATTACA	TAGAAAATCA	GGTTTTACCT	2220

GCCGTTCTTA GAATATTAGA GGCCTTTGGG TACAGGAAAG AAGACCTCAG GTGGCAGAAG 2280
ACTAAACAGA CAGGTCTTAC GGCATGGCTT AACATCAAGA AGAAGTAA 2328

JDF-3

V93R MUTANT: NNN = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS
FOR ARGININE) (SEQ ID NO: 39)

V93E MUTANT: NNN = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) (SEQ ID NO: 40)

ATGATCCTTGACGTTGATTACATCACCGAGAATGGAAAGCCCGTCATCAGGGTCTTCAAGAAGGAGAACGGCGAGTTCA
GGATTGAATACGACCGCGAGTTTCGAGCCCTACTTCTACGCGCTCCTCAGGGACGACTCTGCCATCGAAGAAATCAAAAA
GATAACCGCGGAGAGGCACGGCAGGGTCGTTAAGGTTAAGCGCGCGGAGAAGGTGAAGAAAAAGTTCCCTCGGCAGGTCT
GTGGAGGTCTGGGTCTCTACTTCACGCACCCGCAGGACNNNCCGGCAATCCGCGACAAAATAAGGAAGCACCCCGCGG
TCATCGACATCTACGAGTACGACATAACCTTCGCCAAGCGCTACCTCATAGACAAGGGCCTAATCCCGATGGAAGGTGA
GGAAGAGCTTAAACTCATGTCCTTCGACATCGAGACGCTCTACCACGAGGGAGAAGAGTTTGGAACCGGGCCGATTCTG
ATGATAAGCTACGCCGATGAAAGCGAGGCGCGCGTGATAACCTGGAAGAAGATCGACCTTCCTTACGTTGAGGTTGTCT
CCACCGAGAAGGAGATGATTAAGCGCTTCTTGAGGGTCGTTAAGGAGAAGGACCCGGACGTGCTGATAACATAACAACGG
CGACAACCTTCGACTTCGCCTACCTGAAAAAGCGCTGTGAGAAGCTTGCGGTGAGCTTTACCTCGGGAGGGACGGGAGC
GAGCCGAAGATACAGCGCATGGGGGACAGGTTTGCGGTCGAGGTGAAGGGCAGGGTACACTTCGACCTTTATCCAGTCA
TAAGGCGCACCATAAACCTCCCGACCTACACCCTTGAGGCTGTATACGAGGCGGTTTTTCGGCAAGCCCAAGGAGAAGGT
CTACGCCGAGGAGATAGCCACCGCCTGGGAGACCGGCGAGGGGCTTGAGAGGGTCGCGCGCTACTCGATGGAGGACGCG
AGGGTTACCTACGAGCTTGGCAGGGAGTTCTTCCCGATGGAGGCCAGCTTTCCAGGCTCATCGGCCAAGGCCTCTGGG
ACGTTTCCCGCTCCAGCACCGGCAACCTCGTCGAGTGGTTCTCTCTAAGGAAGGCCTACGAGAGGAACGAACCTCGCTCC
CAACAAGCCCGACGAGAGGGAGCTGGCGAGGAGAAGGGGGGGCTACGcCGGTGGCTACGTCAAGGAGCCGGAGCGGGGA
CTGTGGGACAATATCGTGTATCTAGACTTTCGTAGTCTCTACCTTCAATCATAATCACCCACAACGTCTCGCCAGATA
CGCTCAACCGCGAGGGGTGTAGGAGCTACGACGTTGCCCGGAGGTTCGGTCACAAGTTCTGCAAGGACTTCCCCGGCTT
CATTCCGAGCCTGCTCGGAAACCTGCTGGAGGAAAGGCAGAAGATAAAGAGGAAGATGAAGGCAACTCTCGACCCGCTG
GAGAAGAATCTCCTCGATTACAGGCAACGCCTATCAAGATTCTCGCCAACAGCTACTACGGCTACTACGGCTATGCCA
GGGCAAGATGGTACTGCAGGGAGTGCGCCGAGAGCGTTACGGCATGGGGAAGGGAGTACATCGAAATGGTCATCAGAGA
GCTTGAGGAAAAGTTCGGTTTTAAAGTCCTCTATGCAGACACAGACGGTCTCCATGCCACCATTCCTGGAGCGGACGCT
GAAACAGTCAAGAAAAAGGCAATGGAGTTCTTAAACTATATCAATCCCAAACCTGCCCGGCCTTCTCGAACTCGAATACG
AGGGCTTCTACGTCAGGGGCTTCTTCGTACGAAGAAAAAGTACGCGGTTCATCGACGAGGAGGGCAAGATAACCACGCG
CGGGCTTGAGATAGTCAGGCGCGACTGGAGCGAGATAGCGAAGGAGACGCAGGCGAGGGTTTTTGAGGCGGATACTCAGG
CACGGTGACGTTGAAGAGGCCGTCAGAATTGTCAGGGAAGTCACCGAAAAGCTGAGCAAGTACGAGGTTCCGCCGGAGA
AGCTGGTTATCCACGAGCAGATAACGCGCGAGCTCAAGGACTACAAGGCCACCGGCCCGCACGTAGCCATAGCGAAgCG
TTTGGCCGCCAGAGGTGTTAAATCCGGCCCGAACTGTGATAAGCTACATCGTTCTGAAGGGCTCCGGAAGGATAGGC
GACAGGGCGATTCCCTTCGACGAGTTCGACCCGACGAAGCACAAGTACGATGCGGACTACTACATCGAGAACCAGGTTT
TGCCGGCAGTTGAGAGAATCCTCAGGGCCTTCGGCTACCGCAAGGAAGACCTGCGCTACCAGAAGACGAGGCAGGTCCG
GCTTGCGCGTGGCTGAAGCCGAAGGGGAAGAAGAAGTGA

Figure 13B

>Pfu V93R (SEQ ID NO:41)

MILDVDYITEEGKPVIRLFKKENGKFKIEHDRTFRPYIYALLRDDSKIIEVKKITGERHKGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQDRPTIREKVRHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGK
GPIIMISYADENEAKVITWKNIDLPHYVEVVSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
IGRDGSEPKMQRIGDMTAVEVKGRIFHDLYHVITRTINLPTYTLEAVYEAIIFGKPKEKVYADEIAKAWESGENLERV
AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSSSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRRLRESY
TGGFVKEPEKGLWENIVYLDLFRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFCKDIPGFIPSLLGHLLEERQ
KIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
IDTDGLYATIPGGESEEEIKKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLIIVRRDW
SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAGVK
IKPGMVIGYIVLRGDGPISNRAILAEYDPKKHKYDAEYYIENQVLPVLRILEGFGYRKEDLRYQKTRQVGLTSWL
NIKKs //

>Pfu V93E (SEQ ID NO:42)

MILDVDYITEEGKPVIRLFKKENGKFKIEHDRTFRPYIYALLRDDSKIIEVKKITGERHKGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQDEPTIREKVRHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGK
GPIIMISYADENEAKVITWKNIDLPHYVEVVSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
IGRDGSEPKMQRIGDMTAVEVKGRIFHDLYHVITRTINLPTYTLEAVYEAIIFGKPKEKVYADEIAKAWESGENLERV
AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSSSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRRLRESY
TGGFVKEPEKGLWENIVYLDLFRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFCKDIPGFIPSLLGHLLEERQ
KIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
IDTDGLYATIPGGESEEEIKKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLIIVRRDW
SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAGVK
IKPGMVIGYIVLRGDGPISNRAILAEYDPKKHKYDAEYYIENQVLPVLRILEGFGYRKEDLRYQKTRQVGLTSWL
NIKKs

>Pfu V93R/G387P (SEQ ID NO:43)

MILDVDYITEEGKPVIRLFKKENGKFKIEHDRTFRPYIYALLRDDSKIIEVKKITGERHKGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQDRPTIREKVRHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGK
GPIIMISYADENEAKVITWKNIDLPHYVEVVSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
IGRDGSEPKMQRIGDMTAVEVKGRIFHDLYHVITRTINLPTYTLEAVYEAIIFGKPKEKVYADEIAKAWESGENLERV
AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSSSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRRLRESY
TPGFVKEPEKGLWENIVYLDLFRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFCKDIPGFIPSLLGHLLEERQ
KIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
IDTDGLYATIPGGESEEEIKKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLIIVRRDW
SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAGVK
IKPGMVIGYIVLRGDGPISNRAILAEYDPKKHKYDAEYYIENQVLPVLRILEGFGYRKEDLRYQKTRQVGLTSWL
NIKKs

>Pfu V93R/D141A/E143A (SEQ ID NO:44)

MILDVDYITEEGKPVIRLFKKENGKFKIEHDRTFRPYIYALLRDDSKIIEVKKITGERHKGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQDRPTIREKVRHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGK
GPIIMISYADENEAKVITWKNIDLPHYVEVVSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
IGRDGSEPKMQRIGDMTAVEVKGRIFHDLYHVITRTINLPTYTLEAVYEAIIFGKPKEKVYADEIAKAWESGENLERV
AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSSSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRRLRESY
TGGFVKEPEKGLWENIVYLDLFRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFCKDIPGFIPSLLGHLLEERQ
KIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
IDTDGLYATIPGGESEEEIKKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLIIVRRDW
SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAGVK
IKPGMVIGYIVLRGDGPISNRAILAEYDPKKHKYDAEYYIENQVLPVLRILEGFGYRKEDLRYQKTRQVGLTSWL
NIKKs

Replacement Figure

>Pfu V93E/G387P (SEQ ID NO:45)

MILDVDYITEEGKPVIRLFKKENGKFKIEHDRTFRPYIYALLRDDSKIEEVKKITGERHGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQDEPTIREKVRHAPAVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFEGK
GPIIMISYADENEAKVITWKNIDLPHYVEVSSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
IGRDGSEPKMQRIGDMTAVEVKGRIFHDLYHVITRTINLPTYTLEAVYEAI FGKPKEKVYADEIAKAWESGENLERV
AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSSSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRRLRESY
TPGFVKEPEKGLWENIVYLDLFRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFCKDIPGFIPSLLGHLLEERQ
KIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
IDTDGLYATIPGGESEEEIKKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTCKRYAVIDEEGKVITRGLEIVRRDW
SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAGVK
IKPGMVIGYIVLRGDGPISNRAILAEEDPKKHKYDAEYYIENQVLPVLRILEGFGYRKEDLRYQKTRQVGLTSWL
NIKK

>Pfu V93E/D141A/E143A (SEQ ID NO:46)

MILDVDYITEEGKPVIRLFKKENGKFKIEHDRTFRPYIYALLRDDSKIEEVKKITGERHGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQDRPTIREKVRHAPAVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFEGK
GPIIMISYADENEAKVITWKNIDLPHYVEVSSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
IGRDGSEPKMQRIGDMTAVEVKGRIFHDLYHVITRTINLPTYTLEAVYEAI FGKPKEKVYADEIAKAWESGENLERV
AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSSSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRRLRESY
TGGFVKEPEKGLWENIVYLDLFRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFCKDIPGFIPSLLGHLLEERQ
KIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
IDTDGLYATIPGGESEEEIKKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTCKRYAVIDEEGKVITRGLEIVRRDW
SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAGVK
IKPGMVIGYIVLRGDGPISNRAILAEEDPKKHKYDAEYYIENQVLPVLRILEGFGYRKEDLRYQKTRQVGLTSWL
NIKK

>DEEP VENT V93R (SEQ ID NO:47)

MILDADYITEDGKPIIRIFKKENGFEKVEYDRNFRPYIYALLKDDSQIDEVRKITAERHGKIVRIIDAEKVRKKFLG
RPIEVWRLYFEHPQDRPAIRDKIREHSAVIDIFEYDIPFAKRYLIDKGLIPMEGDEELKLLAFDIETLYHEGEEFAK
GPIIMISYADEEEEAKVITWKKIDLPHYVEVSSSEREMIKRFLKVIREKDPDVIITYNGDSFDLPYLVKRAEKLGIKLP
LGRDGSEPKMQRLGDMTAVEIKGRIFHDLYHVIRRTINLPTYTLEAVYEAI FGKPKEKVYAHEIAEAWETGKGLERV
AKYSMEDAKVTYELGREFFPMEAQLSRLVGQPLWDVSRSSSTGNLVEWYLLRKAYERNELAPNKPDEREYERRRLRESY
AGGYVKEPEKGLWEGLVSLDFRSLYPSIIITHNVSPDTLNREGCREYDVAPEVGHKFCKDFPGFIPSLKRLLLDERQ
EIKRKMASKDPIEKMLDYRQRAIKILANSYGYGYAKARWYCKECAESVTAWGREYIEFVRKELEEKFGFKVLY
IDTDGLYATIPGAKPEEIKKKALEFVDYINAKLPGLLELEYEGFYVRGFFVTCKKYALIDEEGKIITRGLEIVRRDW
SEIAKETQAKVLEAILKHGNVEEAVKIVKEVTEKLSKYEIPPEKLVIEQITRPLHEYKAIGPHVAVAKRLAARGVK
VRPGMVIGYIVLRGDGPISKRAILAEEDLRKHKYDAEYYIENQVLPVLRILEAFGYRKEDLRWQTKQTGLTAWL
NIKK

>DEEP VENT V93E (SEQ ID NO:48)

MILDADYITEDGKPIIRIFKKENGFEKVEYDRNFRPYIYALLKDDSQIDEVRKITAERHGKIVRIIDAEKVRKKFLG
RPIEVWRLYFEHPQDEPAIRDKIREHSAVIDIFEYDIPFAKRYLIDKGLIPMEGDEELKLLAFDIETLYHEGEEFAK
GPIIMISYADEEEEAKVITWKKIDLPHYVEVSSSEREMIKRFLKVIREKDPDVIITYNGDSFDLPYLVKRAEKLGIKLP
LGRDGSEPKMQRLGDMTAVEIKGRIFHDLYHVIRRTINLPTYTLEAVYEAI FGKPKEKVYAHEIAEAWETGKGLERV
AKYSMEDAKVTYELGREFFPMEAQLSRLVGQPLWDVSRSSSTGNLVEWYLLRKAYERNELAPNKPDEREYERRRLRESY
AGGYVKEPEKGLWEGLVSLDFRSLYPSIIITHNVSPDTLNREGCREYDVAPEVGHKFCKDFPGFIPSLKRLLLDERQ
EIKRKMASKDPIEKMLDYRQRAIKILANSYGYGYAKARWYCKECAESVTAWGREYIEFVRKELEEKFGFKVLY
IDTDGLYATIPGAKPEEIKKKALEFVDYINAKLPGLLELEYEGFYVRGFFVTCKKYALIDEEGKIITRGLEIVRRDW
SEIAKETQAKVLEAILKHGNVEEAVKIVKEVTEKLSKYEIPPEKLVIEQITRPLHEYKAIGPHVAVAKRLAARGVK
VRPGMVIGYIVLRGDGPISKRAILAEEDLRKHKYDAEYYIENQVLPVLRILEAFGYRKEDLRWQTKQTGLTAWL
NIKK

>TGO V93R (SEQ ID NO:49)

Replacement Figure

MILDTDYITEDGKPVIRIFKKENGFEFKIDYDRNFEPYIYALLKDDSAIEDVKKITAERHGTTVRVVRAEKVKKKFLG
RPIEVWKLYFTHPQDRPAIRDKIKEHPAVVDIYEYDIPFAKRYLIDKGLIPMEGDEELKMLAFDIETLYHEGEEFAE
GPILMISYADEEGARVITWKNIDL PYVDV VSTEKEMIKRFLKV VKEKDPDVLITYNGDNFDFAYLKKRSEKLGVKFI
LGREGSEP KIQRMGDRFAVEVKGR IHFDLYPVIRRTINLPTYTLEAVYEAIFGQPKEKVYAE EIAQAWETGEGLERV
ARYSMEDAKVTYELGKEFFPMEAQLSRLVGQSLWDVSRSSSTGNLVEWFLLRKAYERNELAPNKPDERELARRRESYA
GGYVKEPERGLWENIVYLDFRSLYPSIIITHNVSPDTLNREGCEEYDVAPQVGHKFCKDFPGFIPSLLGDLLEERQK
VKKMKATIDPIEKLLDYRQRAIKILANSFYGYGYAKARWYCKECAESVTAWGRQYIETTIREIEEKFGFKVLYA
DTDGFFATIPGADAETVKKKAKEFLDYINAKLPGLLELEYEGFYKRGFFVTKKKYAVIDEEDKITTRGLEIVRRDWS
EIAKETQARVLEAILKHGDVEEAVRIVKEVTEKLSKYEVPPEKLV IYEQITRDLKDYKATGPHVAVAKRLAARGIKI
RPGTVISYIVLKSGRIGDRAIPFDEFDPAKHKYDAEYYIENQVLP AVERILRAFGYRKEDLRYQKTRQVGLGAWLK
PKT

>TGO V93E (SEQ ID NO:50)

MILDTDYITEDGKPVIRIFKKENGFEFKIDYDRNFEPYIYALLKDDSAIEDVKKITAERHGTTVRVVRAEKVKKKFLG
RPIEVWKLYFTHPQDEPAIRDKIKEHPAVVDIYEYDIPFAKRYLIDKGLIPMEGDEELKMLAFDIETLYHEGEEFAE
GPILMISYADEEGARVITWKNIDL PYVDV VSTEKEMIKRFLKV VKEKDPDVLITYNGDNFDFAYLKKRSEKLGVKFI
LGREGSEP KIQRMGDRFAVEVKGR IHFDLYPVIRRTINLPTYTLEAVYEAIFGQPKEKVYAE EIAQAWETGEGLERV
ARYSMEDAKVTYELGKEFFPMEAQLSRLVGQSLWDVSRSSSTGNLVEWFLLRKAYERNELAPNKPDERELARRRESYA
GGYVKEPERGLWENIVYLDFRSLYPSIIITHNVSPDTLNREGCEEYDVAPQVGHKFCKDFPGFIPSLLGDLLEERQK
VKKMKATIDPIEKLLDYRQRAIKILANSFYGYGYAKARWYCKECAESVTAWGRQYIETTIREIEEKFGFKVLYA
DTDGFFATIPGADAETVKKKAKEFLDYINAKLPGLLELEYEGFYKRGFFVTKKKYAVIDEEDKITTRGLEIVRRDWS
EIAKETQARVLEAILKHGDVEEAVRIVKEVTEKLSKYEVPPEKLV IYEQITRDLKDYKATGPHVAVAKRLAARGIKI
RPGTVISYIVLKSGRIGDRAIPFDEFDPAKHKYDAEYYIENQVLP AVERILRAFGYRKEDLRYQKTRQVGLGAWLK
PKT

>KOD V93R (SEQ ID NO:51)

MILDTDYITEDGKPVIRIFKKENGFEFKIEYDRTFEPYFYALLKDDSAIEEVKKITAERHGTVVTVKRVEKVQKKFLG
RPVEVWKLYFTHPQDRPAIRDKIREHGAVIDIYEYDIPFAKRYLIDKGLVPMEGDEELKMLAFDIQTLYHEGEEFAE
GPILMISYADEEGARVITWKNVDLPYVDV VSTEREMIKRFLRVVKEKDPDVLITYNGDNFDFAYLKKRCEKLGINF
LGRDGSEP KIQRMGDRFAVEVKGR IHFDLYPVIRRTINLPTYTLEAVYEAIFGQPKEKVYAE EITPAWETGENLERV
ARYSMEDAKVTYELGKEFLPMEAQLSRLIGQSLWDVSRSSSTGNLVEWFLLRKAYERNELAPNKPDEKELARRRQSYE
GGYVKEPERGLWENIVYLDFRSLYPSIIITHNVSPDTLNREGCKEYDVAPQVGHRFCKDFPGFIPSLLGDLLEERQK
IKKKMKATIDPIERKLLDYRQRAIKILANSYYGYGYARARWYCKECAESVTAWGREYITMTIKEIEEKYGFKVIYS
DTDGFFATIPGADAETVKKKAMEFLNYINAKLPGALELEYEGFYKRGFFVTKKKYAVIDEEGKITTRGLEIVRRDWS
EIAKETQARVLEALLKDGDVEKAVRIVKEVTEKLSKYEVPPEKLV IHEQITRDLKDYKATGPHVAVAKRLAARGVKI
RPGTVISYIVLKSGRIGDRAIPFDEFDPTKHKYDAEYYIENQVLP AVERILRAFGYRKEDLRYQKTRQVGLSAWLK
PKGT

>KOD V93E (SEQ ID NO:52)

MILDTDYITEDGKPVIRIFKKENGFEFKIEYDRTFEPYFYALLKDDSAIEEVKKITAERHGTVVTVKRVEKVQKKFLG
RPVEVWKLYFTHPQDEPAIRDKIREHGAVIDIYEYDIPFAKRYLIDKGLVPMEGDEELKMLAFDIQTLYHEGEEFAE
GPILMISYADEEGARVITWKNVDLPYVDV VSTEREMIKRFLRVVKEKDPDVLITYNGDNFDFAYLKKRCEKLGINF
LGRDGSEP KIQRMGDRFAVEVKGR IHFDLYPVIRRTINLPTYTLEAVYEAIFGQPKEKVYAE EITPAWETGENLERV
ARYSMEDAKVTYELGKEFLPMEAQLSRLIGQSLWDVSRSSSTGNLVEWFLLRKAYERNELAPNKPDEKELARRRQSYE
GGYVKEPERGLWENIVYLDFRSLYPSIIITHNVSPDTLNREGCKEYDVAPQVGHRFCKDFPGFIPSLLGDLLEERQK
IKKKMKATIDPIERKLLDYRQRAIKILANSYYGYGYARARWYCKECAESVTAWGREYITMTIKEIEEKYGFKVIYS
DTDGFFATIPGADAETVKKKAMEFLNYINAKLPGALELEYEGFYKRGFFVTKKKYAVIDEEGKITTRGLEIVRRDWS
EIAKETQARVLEALLKDGDVEKAVRIVKEVTEKLSKYEVPPEKLV IHEQITRDLKDYKATGPHVAVAKRLAARGVKI
RPGTVISYIVLKSGRIGDRAIPFDEFDPTKHKYDAEYYIENQVLP AVERILRAFGYRKEDLRYQKTRQVGLSAWLK
PKGT

>VENT V93R (SEQ ID NO:53)

MILDTDYITKDGKPIIRIFKKENGFEKIELDPHFQPYIYALLKDDSAIEEIKAIKGERHGKTVRVLDAVKVRKKFLG
REVEVWKLIFEHPQDRPAMRGKIREHPAVVDIYEYDIPFAKRYLIDKGLIPMEGDEELKLLAFDIETFYHEGDEFGK
GEIIMISYADEEEARVITWKNIDL PYVDVVSNEREMIKRFVQVVKEKDPDVIITYNGDNFDLPYLIKRAEKLGVRLV
LGRDKEHPEPKIQRMGDSFAVEIKGRIHFDLFPVVRRTINLPTYTLEAVYEAVLGKTKSKLGAEIEAAIWETEESMK
KLAQYSMEDARATYELGKEFFPMEAELAKLIGQSVWDVSRSTGNLVEWYLLRVAYARNELAPNKPDEEEYKRRLRT
TYLGGYVKEPEKGLWENIIYLDFRSLYPSIIIVTHNVSPDTLEKEGCKNYDVAPIVGYRFCKDFPGFIP SILGDLIAM
RQDIKKMKSTIDPIEKKMLDYRQRAIKLLANSYYGYMGYPKARWYSKECAESVTAWGRHYIEMTIREIEEKFGFKV
LYADTDGFYATIPGEKPELIKKAKEFLNYINSKLPGLLELEYEGFYLRGFFVTKKRYAVIDEEGRITTRGLEVVRR
DWSEIAKETQAKVLEAILKEGSVEKAVEVVRDVVEKIAKYRVPLEKLV IHEQITRDLKDYKAIGPHVAIAKRLAARG
IKVKPGTIIISYIVLKSGSGKISDRVILLTEYDPRKHKYDPDYIENQVLPVLRILEAFGYRKEDLRYQSSKQTGLDA
WLKR

>VENT V93E (SEQ ID NO:54)

MILDTDYITKDGKPIIRIFKKENGFEKIELDPHFQPYIYALLKDDSAIEEIKAIKGERHGKTVRVLDAVKVRKKFLG
REVEVWKLIFEHPQDEPAMRGKIREHPAVVDIYEYDIPFAKRYLIDKGLIPMEGDEELKLLAFDIETFYHEGDEFGK
GEIIMISYADEEEARVITWKNIDL PYVDVVSNEREMIKRFVQVVKEKDPDVIITYNGDNFDLPYLIKRAEKLGVRLV
LGRDKEHPEPKIQRMGDSFAVEIKGRIHFDLFPVVRRTINLPTYTLEAVYEAVLGKTKSKLGAEIEAAIWETEESMK
KLAQYSMEDARATYELGKEFFPMEAELAKLIGQSVWDVSRSTGNLVEWYLLRVAYARNELAPNKPDEEEYKRRLRT
TYLGGYVKEPEKGLWENIIYLDFRSLYPSIIIVTHNVSPDTLEKEGCKNYDVAPIVGYRFCKDFPGFIP SILGDLIAM
RQDIKKMKSTIDPIEKKMLDYRQRAIKLLANSYYGYMGYPKARWYSKECAESVTAWGRHYIEMTIREIEEKFGFKV
LYADTDGFYATIPGEKPELIKKAKEFLNYINSKLPGLLELEYEGFYLRGFFVTKKRYAVIDEEGRITTRGLEVVRR
DWSEIAKETQAKVLEAILKEGSVEKAVEVVRDVVEKIAKYRVPLEKLV IHEQITRDLKDYKAIGPHVAIAKRLAARG
IKVKPGTIIISYIVLKSGSGKISDRVILLTEYDPRKHKYDPDYIENQVLPVLRILEAFGYRKEDLRYQSSKQTGLDA
WLKR

>JDF-3 V93R (SEQ ID NO:55)

MILDVDYITENGKPVIRVFKKENGFEFRIEYDREFEPYFYALLRDDSAIEEIKKITAERHGRVVKVKRAEKVKKKFLGR
SVEVWVLYFTHPQDRPAIRDKIRKHPAVIDIYEYDIPFAKRYLIDKGLIPMEGEEELKLMSFDIETLYHEGEEFGTGP
ILMISYADESEARVITWKKIDL PYVEVVSTEEKEMIKRFLRVVKEKDPDVLITYNGDNFDFAYLKKRCEKLGVSFTLGR
DGSEPKIQRMGDRFAVEVKGRVHFDLYPVIRRTINLPTYTLEAVYEAVFGKPKEKVYAEIATAWETGEGLERVARYS
MEDARVTYELGREFFPMEAQLSRLIGQGLWDVSRSTGNLVEWFLLRKAYERNELAPNKPDERELARRRGYAGGYVK
EPERGLWDNIVYLDFRSLYPSIIITHNVSPDTLNREGCRSYDVAPEVGHKFCKDFPGFIPSL LGNLEERQKIKRKM
ATLDPLEKNLLDYRQRAIKILANSYYGYGYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYADTDGLHA
TIPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKKYAVIDEEGKITTRGLEIVRRDWSEIAKETQA
RVLEAILRHGDVEEAVRIVREVTEKLSKYEVPPEKLV IHEQITRELKDYKATGPHVAIAKRLAARGVKIRPGTVISYI
VLKGSGRIGDRAIPFDEFDPTKHKYDADYYIENQVLP AVERILRAFGYRKEDLRYQKTRQVGLGAWLKP KGKK

>JDF-3 V93E (SEQ ID NO:56)

MILDVDYITENGKPVIRVFKKENGFEFRIEYDREFEPYFYALLRDDSAIEEIKKITAERHGRVVKVKRAEKVKKKFLGR
SVEVWVLYFTHPQDEPAIRDKIRKHPAVIDIYEYDIPFAKRYLIDKGLIPMEGEEELKLMSFDIETLYHEGEEFGTGP
ILMISYADESEARVITWKKIDL PYVEVVSTEEKEMIKRFLRVVKEKDPDVLITYNGDNFDFAYLKKRCEKLGVSFTLGR
DGSEPKIQRMGDRFAVEVKGRVHFDLYPVIRRTINLPTYTLEAVYEAVFGKPKEKVYAEIATAWETGEGLERVARYS
MEDARVTYELGREFFPMEAQLSRLIGQGLWDVSRSTGNLVEWFLLRKAYERNELAPNKPDERELARRRGYAGGYVK
EPERGLWDNIVYLDFRSLYPSIIITHNVSPDTLNREGCRSYDVAPEVGHKFCKDFPGFIPSL LGNLEERQKIKRKM
ATLDPLEKNLLDYRQRAIKILANSYYGYGYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYADTDGLHA
TIPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKKYAVIDEEGKITTRGLEIVRRDWSEIAKETQA
RVLEAILRHGDVEEAVRIVREVTEKLSKYEVPPEKLV IHEQITRELKDYKATGPHVAIAKRLAARGVKIRPGTVISYI
VLKGSGRIGDRAIPFDEFDPTKHKYDADYYIENQVLP AVERILRAFGYRKEDLRYQKTRQVGLGAWLKP KGKK

Replacement Figure

Figure 14

Tgo 93:

NNN = AGA, AGG, CGA, CGC, CGG, CGT (R)

(NUCLEOTIDE SEQUENCE: SEQ ID NO: 57; AMINO ACID SEQUENCE: SEQ ID NO: 58)

NNN = GAA, GAG (E)

(NUCLEOTIDE SEQUENCE: SEQ ID NO: 59; AMINO ACID SEQUENCE: SEQ ID NO: 60)

5'

atg atc ctc gat aca gac tac ata act gag gat gga aag ccc gtc atc	48
Met Ile Leu Asp Thr Asp Tyr Ile Thr Glu Asp Gly Lys Pro Val Ile	
1 5 10 15	
agg atc ttc aag aag gag aac ggc gag ttc aaa ata gac tac gac aga	96
Arg Ile Phe Lys Lys Glu Asn Gly Glu Phe Lys Ile Asp Tyr Asp Arg	
20 25 30	
aac ttt gag cca tac atc tac gcg ctc ttg aag gac gac tct gcg att	144
Asn Phe Glu Pro Tyr Ile Tyr Ala Leu Leu Lys Asp Asp Ser Ala Ile	
35 40 45	
gag gac gtc aag aag ata act gcc gag agg cac ggc act acc gtt agg	192
Glu Asp Val Lys Lys Ile Thr Ala Glu Arg His Gly Thr Thr Val Arg	
50 55 60	
gtt gtc agg gcc gag aaa gtg aag aag aag ttc cta ggc agg ccg ata	240
Val Val Arg Ala Glu Lys Val Lys Lys Lys Phe Leu Gly Arg Pro Ile	
65 70 75 80	
gag gtc tgg aag ctc tac ttc act cac ccc cag gac nnn ccc gca atc	288
Glu Val Trp Lys Leu Tyr Phe Thr His Pro Gln Asp Xaa Pro Ala Ile	
85 90 95	
agg gac aag ata aag gag cat cct gcc gtt gtg gac atc tac gag tac	336
Arg Asp Lys Ile Lys Glu His Pro Ala Val Val Asp Ile Tyr Glu Tyr	
100 105 110	
gac atc ccc ttc gcg aag cgc tac ctc ata gac aaa ggc tta atc ccg	384
Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro	
115 120 125	
atg gag ggc gac gag gaa ctt aag atg ctc gcc ttc gac atc gag acg	432
Met Glu Gly Asp Glu Glu Leu Lys Met Leu Ala Phe Asp Ile Glu Thr	
130 135 140	
ctc tat cac gag ggc gag gag ttc gcc gaa ggg cct atc ctg atg ata	480
Leu Tyr His Glu Gly Glu Glu Phe Ala Glu Gly Pro Ile Leu Met Ile	
145 150 155 160	
agc tac gcc gac gag gaa ggg gcg cgc gtt att acc tgg aag aat atc	528
Ser Tyr Ala Asp Glu Glu Gly Ala Arg Val Ile Thr Trp Lys Asn Ile	
165 170 175	
gac ctt ccc tat gtc gac gtc gtt tcc acc gag aag gag atg ata aag	576
Asp Leu Pro Tyr Val Asp Val Val Ser Thr Glu Lys Glu Met Ile Lys	
180 185 190	

Replacement Figure

cgc ttc ctc aag gtc gtc aag gaa aag gat ccc gac gtc ctc ata acc	624
Arg Phe Leu Lys Val Val Lys Glu Lys Asp Pro Asp Val Leu Ile Thr	
195 200 205	
tac aac ggc gac aac ttc gac ttc gcc tac ctc aag aag cgc tcc gag	672
Tyr Asn Gly Asp Asn Phe Asp Phe Ala Tyr Leu Lys Lys Arg Ser Glu	
210 215 220	
aag ctc gga gtc aag ttc atc ctc gga agg gaa ggg agc gag ccg aaa	720
Lys Leu Gly Val Lys Phe Ile Leu Gly Arg Glu Gly Ser Glu Pro Lys	
225 230 235 240	
atc cag cgc atg ggc gat cgc ttt gcg gtg gag gtc aag gga agg att	768
Ile Gln Arg Met Gly Asp Arg Phe Ala Val Glu Val Lys Gly Arg Ile	
245 250 255	
cac ttc gac ctc tac ccc gtc att agg aga acg att aac ctc ccc act	816
His Phe Asp Leu Tyr Pro Val Ile Arg Arg Thr Ile Asn Leu Pro Thr	
260 265 270	
tac acc ctt gag gca gta tat gaa gcc atc ttt gga cag ccg aag gag	864
Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Gln Pro Lys Glu	
275 280 285	
aag gtc tac gct gag gag ata gcg cag gcc tgg gaa acg ggc gag gga	912
Lys Val Tyr Ala Glu Glu Ile Ala Gln Ala Trp Glu Thr Gly Glu Gly	
290 295 300	
tta gaa agg gtg gcc cgc tac tcg atg gag gac gca aag gta acc tat	960
Leu Glu Arg Val Ala Arg Tyr Ser Met Glu Asp Ala Lys Val Thr Tyr	
305 310 315 320	
gaa ctc gga aaa gag ttc ttc cct atg gaa gcc cag ctc tcg cgc ctc	1008
Glu Leu Gly Lys Glu Phe Phe Pro Met Glu Ala Gln Leu Ser Arg Leu	
325 330 335	
gta ggc cag agc ctc tgg gat gta tct cgc tcg agt acc gga aac ctc	1056
Val Gly Gln Ser Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu	
340 345 350	
gtc gag tgg ttt ttg ctg agg aag gcc tac gag agg aat gaa ctt gca	1104
Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Leu Ala	
355 360 365	
cca aac aag ccg gac gag agg gag ctg gca aga aga agg gag agc tac	1152
Pro Asn Lys Pro Asp Glu Arg Glu Leu Ala Arg Arg Arg Glu Ser Tyr	
370 375 380	
gcg ggt gga tac gtc aag gag ccc gaa agg gga ctg tgg gag aac atc	1200
Ala Gly Gly Tyr Val Lys Glu Pro Glu Arg Gly Leu Trp Glu Asn Ile	
385 390 395 400	
gtg tat ctg gac ttc cgc tcc ctg tat cct tcg ata ata atc acc cat	1248
Val Tyr Leu Asp Phe Arg Ser Leu Tyr Pro Ser Ile Ile Ile Thr His	
405 410 415	
aac gtc tcc cct gat aca ctc aac agg gag ggt tgt gag gag tac gac	1296

Replacement Figure

Asn	Val	Ser	Pro	Asp	Thr	Leu	Asn	Arg	Glu	Gly	Cys	Glu	Glu	Tyr	Asp		
			420					425					430				
gtg	gct	cct	cag	gta	ggc	cat	aag	ttc	tgc	aag	gac	ttc	ccc	ggc	ttc	1344	
Val	Ala	Pro	Gln	Val	Gly	His	Lys	Phe	Cys	Lys	Asp	Phe	Pro	Gly	Phe		
		435					440					445					
atc	cca	agc	ctc	ctc	gga	gac	ctc	ttg	gag	gag	aga	cag	aag	gta	aag	1392	
Ile	Pro	Ser	Leu	Leu	Gly	Asp	Leu	Leu	Glu	Glu	Arg	Gln	Lys	Val	Lys		
	450					455					460						
aag	aag	atg	aag	gcc	act	ata	gac	cca	atc	gag	aag	aaa	ctc	ctc	gat	1440	
Lys	Lys	Met	Lys	Ala	Thr	Ile	Asp	Pro	Ile	Glu	Lys	Lys	Leu	Leu	Asp		
465					470					475					480		
tac	agg	caa	cga	gca	atc	aaa	atc	ctt	gct	aat	agc	ttc	tac	ggc	tac	1488	
Tyr	Arg	Gln	Arg	Ala	Ile	Lys	Ile	Leu	Ala	Asn	Ser	Phe	Tyr	Gly	Tyr		
				485					490					495			
tac	ggc	tat	gca	aag	gcc	cgc	tgg	tac	tgc	aag	gag	tgc	gcc	gag	agc	1536	
Tyr	Gly	Tyr	Ala	Lys	Ala	Arg	Trp	Tyr	Cys	Lys	Glu	Cys	Ala	Glu	Ser		
			500					505					510				
gtt	acc	gct	tgg	ggc	agg	cag	tac	atc	gag	acc	acg	ata	agg	gaa	ata	1584	
Val	Thr	Ala	Trp	Gly	Arg	Gln	Tyr	Ile	Glu	Thr	Thr	Ile	Arg	Glu	Ile		
		515					520					525					
gag	gag	aaa	ttt	ggc	ttt	aaa	gtc	ctc	tac	gcg	gac	aca	gat	gga	ttt	1632	
Glu	Glu	Lys	Phe	Gly	Phe	Lys	Val	Leu	Tyr	Ala	Asp	Thr	Asp	Gly	Phe		
	530					535					540						
ttc	gca	aca	ata	cct	gga	gcg	gac	gcc	gaa	acc	gtc	aaa	aag	aag	gca	1680	
Phe	Ala	Thr	Ile	Pro	Gly	Ala	Asp	Ala	Glu	Thr	Val	Lys	Lys	Lys	Ala		
545					550					555					560		
aag	gag	ttc	ctg	gac	tac	atc	aac	gcc	aaa	ctg	ccc	ggc	ctg	ctc	gaa	1728	
Lys	Glu	Phe	Leu	Asp	Tyr	Ile	Asn	Ala	Lys	Leu	Pro	Gly	Leu	Leu	Glu		
				565				570					575				
ctc	gaa	tac	gag	ggc	ttc	tac	aag	cgc	ggc	ttc	ttc	gtg	acg	aag	aag	1776	
Leu	Glu	Tyr	Glu	Gly	Phe	Tyr	Lys	Arg	Gly	Phe	Phe	Val	Thr	Lys	Lys		
			580					585					590				
aag	tac	gcg	gtt	ata	gac	gag	gag	gac	aag	ata	acg	acg	cgc	ggg	ctt	1824	
Lys	Tyr	Ala	Val	Ile	Asp	Glu	Glu	Asp	Lys	Ile	Thr	Thr	Arg	Gly	Leu		
		595					600					605					
gaa	ata	gtt	agg	cgt	gac	tgg	agc	gag	ata	gcg	aag	gag	acg	cag	gcg	1872	
Glu	Ile	Val	Arg	Arg	Asp	Trp	Ser	Glu	Ile	Ala	Lys	Glu	Thr	Gln	Ala		
	610					615					620						
agg	gtt	ctt	gag	gcg	ata	cta	aag	cac	ggc	gac	gtt	gaa	gaa	gcg	gta	1920	
Arg	Val	Leu	Glu	Ala	Ile	Leu	Lys	His	Gly	Asp	Val	Glu	Glu	Ala	Val		
625					630					635					640		
agg	att	gtc	aaa	gag	gtt	acg	gag	aag	ctg	agc	aag	tac	gag	gtt	cca	1968	
Arg	Ile	Val	Lys	Glu	Val	Thr	Glu	Lys	Leu	Ser	Lys	Tyr	Glu	Val	Pro		

Replacement Figure

645							650					655					
ccg	gag	aag	ctg	gtc	atc	tac	gag	cag	ata	acc	cgc	gac	ctg	aag	gac	2016	
Pro	Glu	Lys	Leu	Val	Ile	Tyr	Glu	Gln	Ile	Thr	Arg	Asp	Leu	Lys	Asp		
			660					665					670				
tac	aag	gcc	acc	ggg	ccg	cat	gtg	gct	gtt	gca	aaa	cgc	ctc	gcc	gca	2064	
Tyr	Lys	Ala	Thr	Gly	Pro	His	Val	Ala	Val	Ala	Lys	Arg	Leu	Ala	Ala		
		675					680					685					
agg	ggg	ata	aaa	atc	cgg	ccc	gga	acg	gtc	ata	agc	tac	atc	gtg	ctc	2112	
Arg	Gly	Ile	Lys	Ile	Arg	Pro	Gly	Thr	Val	Ile	Ser	Tyr	Ile	Val	Leu		
	690					695					700						
aaa	ggc	tcg	gga	agg	att	ggg	gac	agg	gct	ata	ccc	ttt	gac	gaa	ttt	2160	
Lys	Gly	Ser	Gly	Arg	Ile	Gly	Asp	Arg	Ala	Ile	Pro	Phe	Asp	Glu	Phe		
705					710					715					720		
gac	ccg	gca	aag	cac	aag	tac	gat	gca	gaa	tac	tac	atc	gag	aac	cag	2208	
Asp	Pro	Ala	Lys	His	Lys	Tyr	Asp	Ala	Glu	Tyr	Tyr	Ile	Glu	Asn	Gln		
				725					730					735			
gtt	ctt	cca	gct	gtg	gag	agg	att	ctg	agg	gcc	ttt	ggt	tac	cgt	aaa	2256	
Val	Leu	Pro	Ala	Val	Glu	Arg	Ile	Leu	Arg	Ala	Phe	Gly	Tyr	Arg	Lys		
			740					745					750				
gaa	gat	tta	agg	tat	cag	aaa	acg	cgg	cag	gtt	ggc	ttg	ggg	gcg	tgg	2304	
Glu	Asp	Leu	Arg	Tyr	Gln	Lys	Thr	Arg	Gln	Val	Gly	Leu	Gly	Ala	Trp		
		755					760					765					
cta	aaa	cct	aag	aca	tga											2322	
Leu	Lys	Pro	Lys	Thr													

Figure 17A

Pyrococcus furiosus gene for archaeal histone (Hmf-like)
(ACCESSION No: AB013081)

Nucleotide sequence (SEQ ID NO: 63)

Amino acid sequence (SEQ ID NO: 64)

M	M	G	E	L	P	I	A	P	V	D	R	L	I	R	K	A	G	18
ATG	ATG	GGA	GAA	TTA	CCA	ATT	GCC	CCA	GTT	GAC	AGA	CTT	ATA	AGA	AAG	GCT	GGT	54
A	Q	R	V	S	E	Q	A	A	K	V	L	A	E	H	L	E	E	36
GCT	CAG	AGA	GTT	AGC	GAG	CAA	GCA	GCT	AAG	GTA	CTT	GCA	GAG	CAC	CTT	GAG	GAA	108
K	A	I	E	I	A	K	K	A	V	D	L	A	K	H	A	G	R	54
AAA	GCT	ATT	GAG	ATC	GCA	AAA	AAG	GCA	GTA	GAT	CTT	GCA	AAG	CAC	GCA	GGT	AGA	162
K	T	V	K	V	E	D	I	K	L	A	I	K	S	*				69
AAG	ACC	GTT	AAG	GTC	GAA	GAC	ATT	AAG	CTC	GCA	ATT	AAG	AGC	TGA				207

Figure 17B

(HMF-like)-Taq DNA polymerase fusion protein

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 65)
Amino acid sequence (SEQ ID NO: 64) // Amino acid sequence (SEQ ID NO: 66)

M	M	G	E	L	P	I	A	P	V	D	R	L	I	R	K	A	G	18
ATG	ATG	GGA	GAA	TTA	CCA	ATT	GCC	CCA	GTT	GAC	AGA	CTT	ATA	AGA	AAG	GCT	GGT	54
A	Q	R	V	S	E	Q	A	A	K	V	L	A	E	H	L	E	E	36
GCT	CAG	AGA	GTT	AGC	GAG	CAA	GCA	GCT	AAG	GTA	CTT	GCA	GAG	CAC	CTT	GAG	GAA	108
K	A	I	E	I	A	K	K	A	V	D	L	A	K	H	A	G	R	54
AAA	GCT	ATT	GAG	ATC	GCA	AAA	AAG	GCA	GTA	GAT	CTT	GCA	AAG	CAC	GCA	GGT	AGA	162
K	T	V	K	V	E	D	I	K	L	A	I	K	S					69
AAG	ACC	GTT	AAG	GTC	GAA	GAC	ATT	AAG	CTC	GCA	ATT	AAG	AGC					


```

      G   G   G
    // GGC GGC GGT

V   T   S   G   M   L   P   L   F   E   P   K   G   R   V   L   L   V
GTC ACT AGT GGG ATG CTG CTG CCC CTC TTT GAG CCC AAG GGC CGG GTC CTC CTG GTG

D   G   H   H   L   A   Y   R   T   F   H   A   L   K   G   L   T   T
GAC GGC CAC CAC CTG GGC TAC CGC ACC TTC CAC GCC CTG AAG GGC CTC ACC ACC

S   R   G   E   P   V   Q   A   V   Y   G   F   A   K   S   L   L   K
AGC CGG GGG GAG CCG GTG CAG GCG GTC TAC GGC TTC GCC AAG AGC CTC CTC AAG

A   L   K   E   D   G   D   A   V   I   V   F   D   A   K   A   P
GCC CTC AAG GAG GAC GGG GAC GCG GTG ATC GTG GTC TTT GAC GCC AAG GCC CCC

S   F   R   H   E   A   Y   G   G   Y   K   A   G   R   A   P   T   P
TCC TTC CGC CAC GAG GCC TAC GGG GGG TAC AAG GCG GGC CGG GCC CCC ACG CCA

E   D   F   P   R   Q   L   A   L   I   K   E   L   V   D   L   L   G
GAG GAC TTT CCC CGG CAA CTC GCC CTC ATC AAG GAG CTG GTG GAC CTC CTG GGG

L   A   R   L   E   V   P   G   Y   E   A   D   D   V   L   A   S   L
CTG GCG CGC CTC GAG GTC CCG GGC TAC GAG GCG GAC GAC GTC CTG GCC AGC CTG

A   K   K   A   E   K   E   G   Y   E   V   R   I   L   T   A   D   K
GCC AAG AAG GCG GAA AAG GAG GGC TAC GAG GTC CGC ATC CTC ACC GCC GAC AAA

D   L   Y   Q   L   L   S   D   R   I   H   V   L   H   P   E   G   Y
GAC CTT TAC CAG CTC CTT TCC GAC CGC ATC CAC GTC CTC CAC CCC GAG GGG TAC

L   I   T   P   A   W   L   W   E   K   Y   G   L   R   P   D   Q   W
CTC ATC ACC CCG GCC TGG CTT TGG GAA AAG TAC GGC CTG AGG CCC GAC CAG TGG

A   D   Y   R   A   L   T   G   D   E   S   D   N   L   P   G   V   K
GCC GAC TAC CGG GCC CTG ACC GGG GAC GAG TCC GAC AAC CTT CCC GGG GTC AAG

G   I   G   E   K   T   A   R   K   L   L   E   E   W   G   S   L   E
GGC ATC GGG GAG AAG ACG GCG AGG AAG CTT CTG GAG GAG TGG GGG AGC CTG GAA

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Replacement Figure

A L L L K N L L D R L L K P A I R E K I L
GCC CTC CTC AAG AAC CTG GAC CGG CTG AAG CCC GCC ATC CGG GAG AAG ATC CTG

A H M D D L L K L S W D L A K V R T D
GCC CAC ATG GAC GAT CTG AAG CTC TCC TGG GAC CTG GCC AAG GTG CGC ACC GAC

L P L L E V D F A K R R E P D R E R L
CTG CCC CTG GAG GTG GAC TTC GCC AAA AGG CGG GAG CCC GAC CGG GAG AGG CTT

R A F L L E R L L E F G S L L H E F G L
AGG GCC TTT CTG GAG AGG CTT GAG TTT GGC AGC CTC CTC CAC GAG TTC GGC CTT

L E S P K A L L E E A P W P P E G A
CTG GAA AGC CCC AAG GCC CTG GAG GAG GCC CCC TGG CCC CCG CCG GAA GGG GCC

F V G F V L L S R K E P M W A D L L A
TTC GTG GGC TTT GTG CTT TCC CGC AAG GAG CCC ATG TGG GCC GAT CTT CTG GCC

L A A A R G G L L G L L A K D L S V L
CTG GCC GCC GGC AGG GGG GGC CGG GTC CAC CGG GCC CCC GAG CCT TAT AAA GCC

L R D L K E A R G L L A K D L S V L
CTC AGG GAC CTG AAG GAG GCG CGG GGG CTT CTC GCC AAA GAC CTG AGC GTT CTG

A L R E G L L G L P P G D D P M L L A
GCC CTG AGG GAA GGC CTT GGC CTC CCG CCC GGC GAC GAC CCC ATG CTC CTC GCC

Y L L D P S N T T P E G V A R R Y G
TAC CTC CTG GAC CCT TCC AAC ACC ACC CGG GAG GGG GTG GCC CGG CGC TAC GGC

G E W T E E A G E R A A L S E R L F
GGG GAG TGG ACG GAG GAG GCG GGG GAG CGG GCC CTT TCC GAG AGG CTC TTC

A N L W G R L L E G E R L L L W L Y R
GCC AAC CTG TGG GGG AGG CTT GAG GGG GAG GAG AGG CTC CTT TGG CTT TAC CGG

E V E R P L L S A V L A H M E A T G V
GAG GTG GAG AGG CCC CTT TCC GCT GTC CTC GGC CAC ATG GAG GCC ACG GGG GTG

R L D V A Y L R A L S L E V A E E I
CGC CTG GAC GTG GCC TAT CTC AGG GCC TTG TCC CTG GAG GTG GCC GAG GAG ATC

Replacement Figure

A R L E A E V F R L A G H P F N L N
GCC CGC CTC GAG GCC GAG GTC TTC CGC CTG GCC GGC CAC CCC TTC AAC CTC AAC

S R D Q L E R V L F D E L G L P A I
TCC CGG GAC CAG CTG GAA AGG GTC CTC TTT GAC GAG CTA GGG CTT CCC GCC ATC

G K T E K T G K R S T S A A V L E A
GGC AAG ACG GAG AAG ACC GGC AAG CGC TCC ACC AGC GCC GTC CTG GAG GCC

L R E A H P I V E K I L Q Y R E L T
CTC CGC GAG GCC CAC CCC ATC GTG GAG AAG ATC CTG CAG TAC CGG GAG CTC ACC

K L K S T Y I D P L P D L I H P R T
AAG CTG AAG AGC ACC TAC ATT GAC CCC TTG CCG GAC CTC ATC CAC CCC AGG ACG

G R L H T R F N Q T A T A T G R L S
GGC CGC CTC CAC ACC CGC TTC AAC CAG ACG GCC ACG GCC AGG CTA AGT

S S D P N L Q N I P V R T P L G Q R
AGC TCC GAT CCC AAC CTC CAG AAC ATC CCC GTC CGC ACC CCG CTT GGG CAG AGG

I R R A F I A E E G W L L V A L D Y
ATC CGC CGG GCC TTC ATC GCC GAG GAG GGG TGG CTA TTG GTG GCC CTG GAC TAT

S Q I E L R V L A H L S G D E N L I
AGC CAG ATA GAG CTC AGG GTG CTG GCC CAC CTC TCC GGC GAC GAG AAC CTG ATC

R V F Q E G R D I H T E T A S W M F
CGG GTC TTC CAG GAG GGG CGG GAC ATC CAC ACG GAG ACC GCC AGC TGG ATG TTC

G V P R E A V D P L M R R A A K T I
GGC GTC CCC CGG GAG GCC GTG GAC CCC CTG ATG CGC CGG GCC AAG ACC ATC

N F G V L Y G M S A H R L S Q E L A
AAC TTC GGG GTC CTC TAC GGC ATG TCG GCC CAC CGC CTC TCC CAG GAG CTA GCC

I P Y E E A Q A F I E R Y F Q S F P
ATC CCT TAC GAG GAG GCC CAG GCC TTC ATT GAG CGC TAC TTT CAG AGC TTC CCC

K V R A W I E K T L E E G R R G Y

Replacement Figure

AAG GTG CGG GCC TGG ATT GAG AAG ACC CTG GAG GAG GGC AGG AGG CGG GGG TAC
V E T L F G R R R Y V P D L E A R V
GTG GAG ACC CTC TTC GGC CGC CGC TAC GTG CCA GAC CTA GAG GCC CGG GTG
K S V R E A A E R M A F N M P V Q G
AAG AGC GTG CGG GAG GCG GCC GAG CGC ATG GCC TTC AAC ATG CCC GTC CAG GGC
T A A D L M K L A M V K L F P R L E
ACC GCC GCC GAC CTC ATG AAG CTG GCT ATG GTG AAG CTC TTC CCC AGG CTG GAG
E M G A R M L L Q V H D E L V L E A
GAA ATG GGG GCC AGG ATG CTC CTT CAG GTC CAC GAC GAG CTG GTC CTC GAG GCC
P K E R A E A V A R L A K E V M E G
CCA AAA GAG AGG GCG GAG GCC GTG GCC CGG CTG GCC AAG GAG GTC ATG GAG GGG
V Y P L A V P L E V E V G I G E D W
GTG TAT CCC CTG GCC GTG CCC CTG GAG GTG GAG GTG GGG ATA GGG GAG GAC TGG
L S A K E G I D G R G G G G H H H
CTC TCC GCC AAG GAG GGC ATT GAT GGC CGC GGC GGA GGC CAT CAT CAT CAT
H H *
CAT CAT TAA

Figure 17C

Taq DNA polymerase- (Hmf-like) fusion protein

Nucleotide sequence (SEQ ID NO: 65) //Nucleotide sequence (SEQ ID NO: 63)
Amino acid sequence (SEQ ID NO: 66) /Amino acid sequence (SEQ ID NO: 64)

G G G
GGC GGC GGT

V T S G M L P L F E P K G R V L L V
GTC ACT AGT GGG ATG CTG CCC CTC TTT GAG CCC AAG GGC CGG GTC CTC CTC GTG

D G H H L A Y R T F H A L K G L T T
GAC GGC CAC CAC CTG GGC TAC CGC ACC TTC CAC GCC CTG AAG GGC CTC ACC ACC

S R G E P V Q A V Y G F A K S L L K
AGC CGG GGG GAG CCG GTG CAG GCG GTC TAC GGC TTC GCC AAG AGC CTC CTC AAG

A L K E D G D A V I V V F D A K A P
GCC CTC AAG GAG GAC GGG GAC GCG GTG ATC GTG GTC TTT GAC GCC AAG GCC CCC

S F R H E A Y G G Y K A G R A P T P
TCC TTC CGC CAC GAG GCC TAC GGG GGG TAC AAG GCG GGC CGG GCC CCC ACG CCA

E D F P R Q L A L I K E L V D L L G
GAG GAC TTT CCC CGG CAA CTC GGC CTC ATC AAG GAG CTG GTG GAC CTC CTG GGG

L A R L E V P G Y E A D D V L A S L
CTG GCG CGC CTC GAG GTC CCG GGC TAC GAG GCG GAC GTC CTG GCC AGC CTG

A K K A E K E G Y E V R I L T A D K
GCC AAG AAG GCG GAA AAG GAG GGC TAC GAG GTC CGC ATC CTC ACC GCC GAC AAA

D L Y Q L L S D R I H V L H P E G Y
GAC CTT TAC CAG CTC CTT TCC GAC CGC ATC CAC GTC CTC CAC CCC GAG GGG TAC

L I T P A W L W E K Y G L R P D Q W
CTC ATC ACC CCG GCC TGG CTT TGG GAA AAG TAC GGC CTG AGG CCC GAC CAG TGG

A D Y R A L T G D E S D N L P G V K
GCC GAC TAC CGG GCC CTG ACC GCG GAC GAG TCC GAC AAC CTT CCC GGG GTC AAG

G I G E K T A R K L L E E W G S L E
GGC ATC GGG GAG AAG ACG GCG AGG AAG CTT CTG GAG GAG TGG GGG AGC CTG GAA

A L L K N L D R L K P A I R E K I L
GCC CTC CTC AAG AAC CTG GAC CCG CTG AAG CCC GCC ATC CGG GAG AAG ATC CTG

A H M D D L K L S W D L A K V R T D
GCC CAC ATG GAC GAT CTG AAG CTC TCC TGG GAC CTG GCC AAG GTG CGC ACC GAC

L P L E V D F A K R R E P D R E R L

Replacement Figure

CTG CCC CTG GAG GTG GAC TTC GCC AAA AGG CGG GAG CCC GAC CGG GAG AGG CTT
R A F L E R L E F G S L L H E F G L
AGG GCC TTT CTG GAG AGG CTT GAG TTT GGC AGC CTC CTC CAC GAG TTC GGC CTT
L E S P K A L E E A P W P P E G A
CTG GAA AGC CCC AAG GCC CTG GAG GAG GCC CCC TGG CCC CCG GAA GGG GCC
F V G F V L S R K E P M W A D L L A
TTC GTG GGC TTT GTG CTT TCC CGC AAG GAG CCC ATG TGG GCC GAT CTT CTG GCC
L A A A R G G R V H R A P E P Y K A
CTG GCC GCC GCC AGG GGC GGC CTC CCG GTC CAC CGG GCC CCC GAG CCT TAT AAA GCC
L R D L K E A R G L L A K D L S V L
CTC AGG GAC CTG AAG GAG GCG CGG GGG CTT CTC GCC AAA GAC CTG AGC GTT CTG
A L R E G L G L P P G D D P M L L A
GCC CTG AGG GAA GGC CTT GGC CTC CCG CCC GGC GAC GAC CCC ATG CTC CTC GCC
Y L L D P S N T P E G V A R R Y G
TAC CTC CTG GAC CCT TCC AAC ACC ACC CCC GAG GGG GTG GCC CGG CGC TAC GGC
G E W T E E A G E R A A L S E R L F
GGG GAG TGG ACG GAG GAG GCG GGG GAG CGG GCC CTC TCC GAG AGG CTC TTC
A N L L W G R L E G E E R L L W L Y R
GCC AAC CTG TGG GGG AGG CTT GAG GGG GAG AGG CTC CTT TGG CTT TAC CGG
E V E R P L S A V L A H M E A T G V
GAG GTG GAG AGG CCC CTT TCC GCT GTC CTC GCC CAC ATG GAG GCC ACG GGG GTG
R L D V A Y L R A L S L E V A E E I
CGC CTG GAC GTG GCC TAT CTC AGG GCC TTG TCC CTG GAG GTG GCC GAG GAG ATC
A R L E A E V F R L A G H P F N L N
GCC CGC CTC GAG GCC GAG GTC TTC CGC CTG GCC GGC CAC CCC TTC AAC CTC AAC
S R D Q L E R V L F D E L G L P A I
TCC CGG GAC CAG CTG GAA AGG GTC CTC TTT GAC GAG CTA GGG CTT CCC GCC ATC

Replacement Figure

G K T E K T G K R S T S A A V L E A
GGC AAG ACG GAG AAG ACC GGC AAG CGC TCC ACC AGC GCC GTC CTG GAG GCC

L R E A H P I V E K I L Q Y R E L T
CTC CGC GAG GCC CAC CCC ATC GTG GAG AAG ATC CTG CAG TAC CGG GAG CTC ACC

K L K S T Y I D P L P D L I H P R T
AAG CTG AAG AGC ACC TAC ATT GAC CCC TTG CCG GAC CTC ATC CAC CCC AGG ACG

G R L H T R F N Q T A T A T G R L S
GGC CGC CTC CAC ACC CGC TTC AAC CAG ACG GCC ACG GGC AGG CTA AGT

S S D P N L Q N I P V R T P L G Q R
AGC TCC GAT CCC AAC CTC CAG AAC ATC CCC GTC CGC ACC CCG CTT GGG CAG AGG

I R R A F I A E E G W L L V A L D Y
ATC CGC CGG GCC TTC ATC GCC GAG GAG GGG TGG CTA TTG GTG GCC CTG GAC TAT

S Q I E L R V L A H L S G D E N L I
AGC CAG ATA GAG CTC AGG GTG CTG GCC CAC CTC TCC GGC GAC GAG AAC CTG ATC

R V F Q E G R D I H T E T A S W M F
CGG GTC TTC CAG GAG GGG CGG GAC ATC CAC ACG GAG ACC GCC AGC TGG ATG TTC

G V P R E A V D P L M R R A A K T I
GGC GTC CCC CGG GAG GCC GTG GAC CCC CTG ATG CGC CGG GCC AAG ACC ATC

N F G V L Y G M S A H R L S Q E L A
AAC TTC GGG GTC CTC TAC GGC ATG TCG GCC CAC CGC CTC TCC CAG GAG CTA GCC

I P Y E E A Q A F I E R Y F Q S F P
ATC CCT TAC GAG GAG GCC CAG GCC TTC ATT GAG CGC TAC TTT CAG AGC TTC CCC

K V R A W I E K T L E E G R R G Y
AAG GTG CGG GCC TGG ATT GAG AAG ACC CTG GAG GAG GCC AGG AGG CGG GGG TAC

V E T L F G R R Y V P D L E A R V
GTG GAG ACC CTC TTC GGC CGC CGC TAC GTG CCA GAC CTA GAG GCC CGG GTG

K S V R E A A E R M A F N M P V Q G
AAG AGC GTG CGG GAG GCC GCG ATG GCC TTC AAC ATG CCC GTC CAG GGC

Replacement Figure

T	A	A	D	L	M	K	L	A	M	V	K	L	F	P	R	L	E		
ACC	GCC	GCC	GAC	CTC	ATG	AAG	CTG	GCT	ATG	GTG	AAG	CTC	TTC	CCC	AGG	CTG	GAG		
E	M	G	A	R	M	L	L	Q	V	H	D	E	L	V	L	E	A		
GAA	ATG	GGG	GCC	AGG	ATG	CTC	CTT	CAG	GTC	CAC	GAC	GAG	CTG	GTC	CTC	GAG	GCC		
P	K	E	R	A	E	A	V	A	R	L	A	K	E	V	M	E	G		
CCA	AAA	GAG	AGG	GCG	GAG	GCC	GTG	GCC	CGG	CTG	GCC	AAG	GAG	GTC	ATG	GAG	GGG		
V	Y	P	L	A	V	P	L	E	V	E	V	G	I	G	E	D	W		
GTG	TAT	CCC	CTG	GCC	GTG	CCC	CTG	GAG	GTG	GAG	GTG	GGG	ATA	GGG	GAG	GAC	TGG		
L	S	A	K	E	G	I	D	G	R	G	G	G	G	H	H	H	H		
CTC	TCC	GCC	AAG	GAG	GGC	ATT	GAT	GGC	CGC	GGC	GGA	GGC	GGG	CAT	CAT	CAT	CAT		
H	H	//																	
CAT	CAT	//																	
M	M	G	E	L	P	I	A	P	V	D	R	L	I	R	K	A	G	18	
ATG	ATG	GGA	GAA	TTA	CCA	ATT	GCC	CCA	GTT	GAC	AGA	CTT	ATA	AGA	AAG	GCT	GGT	54	
A	Q	R	V	S	E	Q	A	A	K	V	L	A	E	H	L	E	E	36	
GCT	CAG	AGA	GTT	AGC	GAG	CAA	GCA	GCT	AAG	GTA	CTT	GCA	GAG	CAC	CTT	GAG	GAA	108	
K	A	I	E	I	A	K	K	A	V	D	L	A	K	H	A	G	R	54	
AAA	GCT	ATT	GAG	ATC	GCA	AAA	AAG	GCA	GTA	GAT	CTT	GCA	AAG	CAC	GCA	GGT	AGA	162	
K	T	V	K	V	E	D	I	K	L	A	I	K	S	*					69
AAG	ACC	GTT	AAG	GTC	GAA	GAC	ATT	AAG	CTC	GCA	ATT	AAG	AGC	TGA					

Figure 17D

Pfu DNA Polymerase (WT) -(HMF-like) fusion protein

Nucleotide sequence (SEQ ID NO: 61) //Nucleotide sequence (SEQ ID NO: 63)

//

ccctggtcct gggtcacat atatgttctt actgccttt atgaagaatc cccagtcgc
tctaacctgg gttatagtga caaatcttcc tccaccaccg cccaagaagg ttatttctat
caactctaca cctccccctat tttctctctt atgagatttt taagtatagt tatagagaag
gttttatact ccaaactgag ttagtagata tgtggggagc ataatgattt tagatgtgga
ttacataact gaagaaggaa aacctgttat taggctattc aaaaaagaga acgaaaaatt
taagatagag catgatagaa cttttagacc atacatttac gctcttctca gggatgattc
aaagattgaa gaagttaaga aaataacggg ggaaaggcat ggaaagattg tgagaattgt
tgatgtagag aagggtgaga aaaagtctct cggcaagcct attaccgtgt ggaaacttta
tttggaacat cccaagatg tcccactat tagagaaaaa gttagagaac atccagcagt
tgtggacatc ttcgaatacg atattccatt tgcaaaagaga tacctcatcg acaaaggcct
aataccaatg gagggggaag aagagctaaa gattcttgcc ttcgatatag aaaccctcta
tcacgaaggga gaagagtctg gaaaaggccc aattataatg attagttatg cagatgaaaa
tgaaagcaaa gtgattactt ggaaaaacat agatcttcca tacgttgagg ttgtatcaag
cgagagagag atgataaaga gatttctcag gattatcagg gagaaggatc ctgacattat
agttacttat aatggagact cattcgactt cccatattta gcgaaaaagg cagaaaaact
tgggattaaa ttaaccattg gaagagatgg aagcgagccc aagatgcaga gaataggcga
tatgacggct gtagaagtca agggaagaat acatttcgac ttgtatcatg taataacaag
gacaataaat ctccaacat acacactaga ggctgtatat gaagcaattt ttggaaagcc
aaaggagaag gtatacgccg acgagatagc aaaagcctgg gaaagtggag agaaccctga
gagagttgcc aaatactcga tggaagatgc aaaggcaact tatgaactcg ggaaagaatt

Replacement Figure

ccttccaatg gaaattcagc tttcaagatt agttggacaa cctttatggg atgtttcaag
gtcaagcaca gggaaccttg tagagtgggt cttacttagg aaagcctacg aaagaaaacga
agtagctcca aacaagccaa gtgaagagga gtatcaaga aggctcaggg agagctacac
agggtgattc gttaaagagc cagaaaaagg gttgtgggaa aacatagtat acctagattt
tagagcccta tatccctcga ttataattac ccacaatgtt tctcccgata ctctaaatct
tgagggatgc aagaactatg atatcgctcc tcaagtaggc cacaagtctt gcaaggacat
ccctgggttt ataccaagtc tcttgggaca tttgttagag gaaagacaaa agattaagac
aaaaatgaag gaaactcaag atcctataga aaaaatactc cttgactata gacaaaaagc
gataaaaact ttagcaaat ctttctacgg atattatggc tatgcaaaaag caagatggta
ctgtaaggag tgtgctgaga gcgttactgc ctggggaaga aagtacatcg agttagtatg
gaaggagctc gaagaaaaagt ttggatttaa agtcctctac attgacactg atggtctcta
tgcaactatc ccaggaggag aaagtgagga aataaagaaa aaggctctag aatttgtaaa
atacataaat tcaaaagctcc ctggactgct agagcttgaa tatgaagggt ttataagag
gggatcttc gtacgaaga agaggtatgc agtaatagat gaagaaggaa aagtcattac
tcgtgggtta gagatagtta ggagagattg gagtgaaatt gcaaaaagaaa ctcaagctag
agttttggag acaatactaa aacacggaga tgttgaagaa gctgtgagaa tagtaaaaga
agtaatacaa aagcttgcca attatgaaat tccaccagag aagctcgcaa tatatgagca
gataacaaga ccattacatg agtataaggc gataggctct cacgtagctg ttgcaaaagaa
actagctgct aaaggagtta aaataaagcc aggaatggta attggataca tagtacttag
aggcgatggc ccaattagca atagggcaat tctagctgag gaatacgatc ccaaaaagca
caagtatgac gcagaatat acattgagaa ccagggtctt ccagcggtag ttaggatatt

Replacement Figure

```
ggagggattt ggatacagaa aggaagacct cagataccaa aagacaagac aagtcggcct
aacttcctgg cttaacatta aaaatccta gaaagcgat agatatcaac ttttatctctt
tctaaccttt ttctatgaaa gaagaactga gcaggaatta ccagttcttc cgttatttta
tgggtaatta aaaaccatg ctcttgggag aatcttcgaa taaaatccct aacttcaggc
tttgctaagt gaatagaata aacaacatca ctcaattcaa acgccttcgt tagaaatggt
ctatctgcat gcttctcttg ctcggaanng gaggattcat aacaacagta tcaacattct
cagagaattg agaaacatca gaaactttga ctctacaac atttctaact ttgcaactct
tcaagatttt ctaaaagaat tttaacggcc tcctcgtcaa ttctgcagac gtagatcttt
tttgctccaa gcagagccgc tccaatggat aacacccctg ttcccgacc caagtccgct
acaatttttt ccttgtatct cctaattgtat aagcaagcca aaggagagta gatgctacct
ttccgggagt ttgtattgc tctagccaag gtcttgggatt ttggaatcct ttaactctgg
aaagtataat ttcaagctcc ttcttcttca tgacagatga aaaattgttt tgtctctttt
taacttttac agaaataact gtctcaaatt atgacaactc ttgacatttt tacttcatta
ccagggtaat gtttttaagt atgaaatttt tctttcatag aggaggnnnn nngtcctctc
ctcgatttcc ttggtttgtc tccatatgat aagcttccaa agtgggtgtt cagactttta
gacactcaaa taccagacga caatggtgtg ctcaactcaag ccccatatgg gttgagaaaa
gtagaagcgg cactactcag atgcttcccc aggaatgagg ttgttgtagc tcntcccnga
aagattgaga tgttcttgg //
```

ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT	54
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA	108
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA	162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA	

Replacement Figure

Figure 17E

(Hmf-like) - Pfu DNA Polymerase (WT) fusion protein

Nucleotide sequence (SEQ ID NO: 63) //Nucleotide sequence (SEQ ID NO: 61)

ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT	54
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA	108
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA	162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC //	

ccctggtcct gggtcacat atatgttctt actgccttt atgaagaatc cccagtcgc

tctaacctgg gttatagtga caaatcttcc tccaccaccg cccaagaagg ttatttctat

caactctaca cctccccctat tttctctctt atgagatttt taagtatagt tatagagaag

gttttatact ccaaaactgag ttagtagata tgtggggagc ataatgattt tagatgtgga

ttacataact gaagaaggaa aacctgttat taggctattc aaaaaagaga acgaaaaatt

taagatagag catgatagaa ctttttagacc atacatttac gctcttctca gggatgattc

aaagattgaa gaagttaaga aaataacggg ggaaaggcat ggaaagattg tgagaattgt

tgatgtagag aagggtgaga aaaagtttct cggcaagcct attaccgtgt ggaaacttta

tttggaacat cccaagatg ttcccactat tagagaaaaa gttagagaac atccagcagt

tgtggacatc ttcgaatacg atattccatt tgcaaaagaga tacctcatcg acaaaggcct

aataccaatg gagggggaag aagagctaaa gattcttgcc ttcgatatag aaaccctcta

tcacgaagga gaagagtgtg gaaaaggccc aattataatg attagttatg cagatgaaaa

tgaaagcaag gtgattactt ggaaaaacat agatcttcca tacgttgagg ttgtatcaag

tcgtggttta gagatagtta ggagagattg gagtgaatt gcaaaagaaa ctcaagctag
agttttggag acaatactaa aacacggaga tgttgaagaa gctgtgagaa tagtaaaaga
agtaatacaa aagcttgcca attatgaaat tccaccagag aagctcgcaa tatatgagca
gataacaaga ccattacatg agtataaggc gataggctct cacgtagctg ttgcaaaagaa
actagctgct aaaggagtta aaataaagcc aggaatggta attggataca tagtacttag
aggcgatggt ccaattagca atagggcaat tctagctgag gaatacgatc ccaaaaagca
caagtatgac gcagaatatt acattgagaa ccaggttctt ccagcggtag ttaggatatt
ggagggattt ggatacacagaa aggaagacct cagataccaa aagacaagac aagtcggcct
aacttcctgg cttaacatta aaaaatccta gaaaagcgat agatatcaac ttttatctt
tctaaccttt ttctatgaaa gaagaactga gcaggaatta ccagttcttc cgttatttta
tgggtaatta aaaaccatg ctcttgggag aatcttcgaa taaaatccct aacttcaggc
tttgctaagt gaatagaata aacaacatca ctacttcaa acgccttctg tagaaatggt
ctatctgcat gcttctcttg ctcggaanng gaggattcat aacaacagta tcaacattct
cagagaattg agaaacatca gaaactttga ctctacaac atttctaact ttgcaactct
tcaagatttt ctaaaagaat tttaacggcc tcctcgtcaa tttcgacgac gtagatcttt
tttgctccaa gcagagccgc tccaatggat aacacccctg ttcccgacc caagtccgct
acaatttttt ccttgatatct cctaattgtat aagcaagcca aaggagagta gatgctacct
ttccgggagt ttgtatttgc tctagccaag gtttgggatt ttggaatcct ttaactctgg
aaagtataat ttcaagctcc ttcttcttca tgacagatga aaaattgttt tgtctctttt
taacttttac agaaaataact gtctcaaatt atgacaactc ttgacatttt tacttcatta

Replacement Figure

cgagagagag atgataaaga gatttctcag gattatcagg gagaaggatc ctgacattat
agttacttat aatggagact cattcgactt cccatattta gcgaaaaggg cagaaaaact
tgggattaaa ttaaccattg gaagagatgg aagcgagccc aagatgcaga gaataggcga
tatgacggct gtagaagtca agggaagaat acatttcgac ttgtatcatg taataacaag
gacaataaat ctcccaacat acacactaga ggctgtatat gaagcaattt ttggaaagcc
aaaggagaag gtatacgccg acgagatagc aaaagcctgg gaaagtgag agaaccttga
gagagtggcc aaataactcga tggaagatgc aaaggcaact tatgaactcg ggaaagaatt
ccttccaatg gaaattcagc tttcaagatt agttggaca ctttatggg atgtttcaag
gtcaagcaca gggaaccttg tagagtgggt cttacttagg aaagcctacg aaagaaacga
agtagctcca aacaagccaa gtgaagagga gtatcaaaagc aggtcaggg agagctacac
agggtgattc gttaaagagc cagaaaaggg gttgtgggaa aacatagtat acctagattt
tagagcccta tatccctcga ttataattac ccacaatgtt tctcccgata ctctaaatct
tgagggatgc aagaactatg atatcgctcc tcaagtaggc cacaagtctt gcaaggacat
ccctggtttt ataccaagtc tcttgggaca ttgtttagag gaaagacaaa agattaagac
aaaaatgaag gaaactcaag atcctataga aaaaatactc cttgactata gacaaaaagc
gataaaactc ttagcaaatt ctttctacgg atattatggc tatgcaaaaag caagatggta
ctgtaaggag tgtgctgaga gcgttactgc ctgggggaaga aagtacatcg agttagtatg
gaaggagctc gaagaaaaagt ttggatttaa agtcctctac attgacactg atggtctcta
tgcaactatc ccaggaggag aaagtgagga aataaaagaa aaggctctag aatttgtaaa
atacataaat tcaaagctcc ctggactgct agagcttgaa tatgaaggggt ttataagag
gggattcttc gttacgaaga agaggtatgc agtaatagat gaagaaggaa aagtcattac

Replacement Figure

ccagggtaat gtttttaagt atgaaatttt tctttcatag aggaggnnnn nngtcctctc
ctcgatttcc ttggttgtgc tccatatgat aagtttcaa agtgggtgtt cagactttta
gacactcaaa taccagacga caatgggtgtg ctactcaag ccccatatgg gttgagaaaa
gtagaagcgg cactactcag atgcttcccc aggaatgagg ttgtgttagc tcntcccnga
aagattgaga tgttcttgg // TGA

Figure 17F

(Hmf-like) - pfu DNA POLYMERASE (V93 R OR E) fusion protein

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 27)
Nucleotide sequence (SEQ ID NO: 63) //Nucleotide sequence (SEQ ID NO: 28)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT	54
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA	108
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA	162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC //	

//ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAA TAACGGGGGA AAGCATGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATXXXC CCACTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTCG AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCCTC 420
GATATAGAAA CCCCTCTATCA CGAAGGAGAA GAGTTGGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAAATGA AGCAAAGGTG ATTACTTGGG AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCC ATATTAGCG 660
AAAAGGGCAG AAAAACTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720

ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTGG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
GAACTCGGGA AAGAATTCCCT TCCAATGGAA ATTCAAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAAGT AGCTCCAAAC AAGCCAAAGT AAGAGAGTA TCAAAGAAGG 1140
CTCAGGGAGA GCTACACAGG TGGATTTCGT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCCT TCTACGGATA TTATGGCTAT 1500
GCAAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGAAGAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAG 1680
GCTCTAGAAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAATATGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAAGCCA TTACATGAGT ATAAGCGGAT AGGTCCCTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAA TAAAGCCAGG AATGGTAAT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGCCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTCTTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAAGG AAGACCTCAG ATACCAAAAG 2280
ACAAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAA AATCC // 2328
// TGA

Figure 17G

PFU DNA POLYMERASE (V93 R OR E) -(Hmf-like) fusion protein

Nucleotide sequence (SEQ ID NO: 27) // Nucleotide sequence (SEQ ID NO: 63)

Nucleotide sequence (SEQ ID NO: 28) // Nucleotide sequence (SEQ ID NO: 63)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)

V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAA 60

AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120

CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAA TAACGGGGA AAGGCATGA 180

AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240

ACCGTGTGGA AACTTTATT TTGGAACATCCC CAAGATXXXC CCACTATTAG AGAAAAAGTT 300

AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAAGAGATAC 360

CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCCTC 420

GATATAGAAA CCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCAAT TATAATGATT 480

AGTTATGCAG ATGAAAAATGA AGCAAAGGTG ATTACTTGGG AAAACATAGA TCTTCCATAC 540

GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600

AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTTCC ATATTTAGCG 660

AAAAGGCAG AAAA ACTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720

ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTTCGACTTG 780

TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840

GCAATTTTGG GAAAGCCAAA GGAGAAAGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900

AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960

GAACTCGGGA AAGAATTCCT TCCAATGGAA ATTCAAGCTTT CAAGATTAGT TGGACAACCT 1020

TTATGGGATG TTTC AAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAA 1080

GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAAG 1140

CTCAGGGAGA GCTACACAGG TGGATTTCGT AAAGAGCCAG AAAAGGGGTT GTGGGAAAA 1200

ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260

CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320

AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380

AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAA AATACTCCTT 1440

GACTATAGAC AAAAGCGAT AAAACTCTTA GCAAAATCTT TCTACGGATA TTATGGCTAT 1500

GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTA CTGCCCTG GGGAAAGAA 1560

TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620

GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680

GCTCTAGAA TGTGAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740

GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800

GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAAATTGCA 1860

AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAC ACGGAGATGT TGAAGAGCT 1920

GTGAGAAATAG TAAAAGAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980

CTCGCAATAT ATGAGCAGAT AACAAAGACCA TTACATGAGT ATAAGGCGAT AGTCCCTCAC 2040

GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAA TAAAGCCAGG AATGGTAATT 2100

GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160

TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTCTTCCA 2220

Replacement Figure

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GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAG 2280
ACAAGACAAG TCGGCCCTAAC TTCCTGGCTT AACATTAAAA AATCC // 2328

ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA

```

Figure 17H

PFU DNA POLYMERASE (G387P/V93R OR E) -(Hmf-like) fusion protein

Nucleotide sequence (SEQ ID NO: 29) // Nucleotide sequence (SEQ ID NO: 63)

Nucleotide sequence (SEQ ID NO: 30) // Nucleotide sequence (SEQ ID NO: 63)

G387P Mutant (CCN is the codon for Proline where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

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ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAA 60
AAAGAGAACG GAAAATTAA GATAGAGCAT GATAGAAGCTT TTAGACCATA CATTACGCT 120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAA TAACGGGGGA AAGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATXXXC CCACTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTGTC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCCTC 420
GATATAGAAA CCCTCTATCA CGAAGGAGAA GAGTTTGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGA AAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCT ATATTTAGCG 660
AAAAGGCGAG AAAAAGCTTG GATTAAATTA ACCATTGGA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAAATACA TTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTGG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAA AGCTGGGAA 900
AGTGAGAGAG ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAA GGCAACTTAT 960
GAACTCGGGA AAGAATTCCT TCCAATGGAA ATTCAAGCTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140

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Replacement Figure

CTCAGGGAGA GCTACACACC NGGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAA AAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAAAGCGAT AAAACTCTTA GCAAATCTTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTTACTGCCCTG GGAAGAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAAA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGA AATTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAC ACGGAGATGT TGAAGAAAGCT 1920
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAAGACCA TTACATGAGT ATAAGGCGAT AGTCCCTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGTTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCCTTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTGGA TACAGAAAGG AAGACCTCAG ATACCAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC // 2328

ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA

Figure 17I

(Hmf-like) - PFU DNA POLYMERASE (G387P/V93R OR E) fusion protein

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 29)

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 30)

G387P Mutant (CCN is the codon for Proline where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54

GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC //

//ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60
AAAGAGAACG GAAAAATTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAA TAACGGGGA AAGCATGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATXXXC CCACTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTCG AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420
GATATAGAAA CCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGCCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAAATGA AGCAAGGTG ATTACTTGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCC ATATTAGCG 660
AAAAGGGCAG AAAA~~ACT~~TGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGCGTGTG GAAGTCAAGG GAAGAATACA TTTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
GAACTCGGGA AAGAATTCCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140
CTCAGGGAGA GCTACACACC NGGATTTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATCTTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTA~~CT~~GCCCTG GGAAGAGAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGA~~AA~~TTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAAGACCA TTACATGAGT ATAAGGCCGAT AGTCCCTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAAACCA GGTTCCTTCCA 2220

Replacement Figure

GGGCTACTTA GGATATTGGA GGGATTGTGA TACAGAAAGG AAGACCTCAG ATACCAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC //TAG 2328

Figure 17J

(HMF-LIKE) -PFU DNA POLYMERASE(D141A/E143A/V93R OR E) fusion protein

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 31)

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 32)

D141A/E143A Mutant (GCN is the codon for alanine where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATG	ATG	GGA	GAA	TTA	CCA	ATT	GCC	CCA	GTT	GAC	AGA	CTT	ATA	AGA	AAG	GCT	GGT	54
GCT	CAG	AGA	GTT	AGC	GAG	CAA	GCA	GCT	AAG	GTA	CTT	GCA	GAG	CAC	CTT	GAG	GAA	108
AAA	GCT	ATT	GAG	ATC	GCA	AAA	AAG	GCA	GTA	GAT	CTT	GCA	AAG	CAC	GCA	GGT	AGA	162
AAG	ACC	GTT	AAG	GTC	GAA	GAC	ATT	AAG	CTC	GCA	ATT	AAG	AGC	//				

//ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60
AAAGAGAACG GAAAATTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAA TAACGGGGA AAGCATGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATXXXC CCACTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTGTC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420
GCNATAGCNA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAAATGA AGCAAAGGTG ATTACTTGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCT ATATTTAGCG 660
AAAAGGGCAG AAAAAGCTTG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAAGAATACA TTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTGG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
GAACTCGGGA AAGAAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020

TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140
CTCAGGGAGA GCTACACA GGT⁼GGATTGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTTCT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTA^{CT}GCCTG GGAAGAAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAAATTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGTCCCTCAC 2040
GTAGCTGTTG CAAAGAACT AGCTGCTAAA GGAGTTAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGC^{CA}ATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTCTTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTGGA TACAGAAAAG AAGACCTCAG ATACCAAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAA AATCC // 2328

TGA

Figure 17K

PFU DNA POLYMERASE (D141A/E143A/V93R OR E) - (HMF-LIKE) fusion protein

Nucleotide sequence (SEQ ID NO: 31) // Nucleotide sequence (SEQ ID NO: 63)

Nucleotide sequence (SEQ ID NO: 32) // Nucleotide sequence (SEQ ID NO: 63)

D141A/E143A Mutant (GCN is the codon for alanine where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTACGCT 120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAAGAAA AGTTTCTCGG CAAGCCATT 240

Replacement Figure

ACCGTGTGGA AACTTTTATTT GGAACATCCC CAAGATXXXC CCACTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420
GCNATAGCNA CCTCTATCA CGAAGGAGAA GAGTTTGAA AAGGCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGA AAACATAGA TCTTCCATAC 540
GTTGAGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTTCC ATATTTAGCG 660
AAAAGGCGAG AAAAAGTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGCGGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTGG GAAAGCCAAA GGAGAAAGTA TACGCCGACG AGATAGCAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
GAACTCGGGA AAGAATTCCCT TCCAATGGAA ATTCAAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGAGTA TCAAAGAAGG 1140
CTCAGGGAGA GCTACACA GTGGATTTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTATA CCAAGTCTCT TGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCCT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTAAGTCCCTG GGGAAGAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAAG GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAAATTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAAATAG TAAAGAAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAAG 1980
CTCGCAATAT ATGAGCAGAT AACAGACCA TTACATGAGT ATAAGGCGAT AGGTCCCTAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAA GGCAATTCT AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGCATTTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTCTTTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAAG AAGACCTCAG ATACCAAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC // 2328

ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA

Replacement Figure

Figure 17L

KOD DNA POLYMERASE - (HMF-like) fusion protein

Nucleotide sequence (SEQ ID NO: 33) // Nucleotide sequence (SEQ ID NO: 63)
Nucleotide sequence (SEQ ID NO: 34) // Nucleotide sequence (SEQ ID NO: 63)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
ATGATCCTCG ACACTGACTA CATAACCGAG GATGGAAAGC CTGTCATAAG AATTTCAAG 60
AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT TTGAACCCCTA CTTCTACGCC 120
CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAAAG TAACCGCCGA GAGCACGGG 180
ACGGTTGTAA CGGTTAAGCG GGTGAAAAG GTTCAGAAGA AGTTCCTCGG GAGACCAGTT 240
GAGGTCGTGA AACTCTACTT TACTCATCCG CAGGACXXXC CAGCGATAAG GGACAAAGATA 300
CGAGAGCATC CAGCAGTTAT TGACATCTAC GAGTACGACA TACCCTTCGC CAAGCGCTAC 360
CTCATAGACA AGGGATTAGT GCCAATGGAA GCGACGAGG AGCTGAAAAT GCTCGCCTTC 420
GACATTGAAA CTCTCTACCA TGAGGGCGAG GAGTTCGCCG AGGGCCCAAT CCTTATGATA 480
AGCTACGCCG ACGAGGAAGG GGCCAGGGTG ATAACTTGA AGAACGTGA TCTCCCCTAC 540
GTTGACGTCG TCTCGACGGA GAGGGAGATG ATAAAGCGCT TCCTCCGTGT TGTGAAGGAG 600
AAAGACCCCG ACGTTCTCAT AACCTACAAC GCGACAAC TCGACTTCGC CTATCTGAAA 660
AAGCGCTGTG AAAAGCTCGG AATAAACTTC GCCCTCGGAA GGGATGGAAG CGAGCCGAAG 720
ATTGAGAGGA TGGCGACAG GTTTGCCGTC GAAGTGAAGG GACGGATACA CTTGATCTC 780
TATCCTGTGA TAAGACGGAC GATAAACCTG CCCACATACA CGCTTGAGGC CGTTTATGAA 840
GCCGTCCTCG GTCAGCCGAA GGAGAAGGTT TACGCTGAGG AAATAACCAAC AGCCTGGAA 900
ACCGGCGAGA ACCTTGAGAG AGTCGCCCGC TACTCGATGG AAGATGCGAA GGTCACATAC 960
GAGCTTGGGA AGGAGTTCCT TCCGATGGAG GCCCAGCTTT CTCGCTTAAT CGGCCAGTCC 1020
CTCTGGGACG TCTCCCGCTC CAGCACTGGC AACCTCGTTG AGTGGTTCTT CCTCAGGAAG 1080
GCCATAGAGA GGAATGAGCT GGCCCCGAAC AAGCCCGATG AAAAGGAGCT GGCCAGAAGA 1140
CGGCAGAGCT ATGAAGGAGG CTATGTAAAA GAGCCCGAGA GAGGGTTGTG GGAGAACATA 1200
GTGTACCTAG ATTTTAGATC CCTGTACCCC CTCAATCATCA TCACCCACAA CGTCTCGCCG 1260
GATACGCTCA ACAGAGAAGG ATGCAAGGAA TATGACGTTG CCCACAGGT CGGCCACCGC 1320
TTCTGCAAGG ACTTCCCAGG ATTTATCCCG AGCCTGCTTG GAGACCTCCT AGAGGAGAGG 1380
CAGAAGATAA AGAAGAAGAT GAAGGCCACG ATTGACCCGA TCGAGAGGAA GCTCCTCGAT 1440
TACAGGCAGA GGGCCATCAA GATCCTGGCA AACAGCTACT ACGTTACTA CGGCTATGCA 1500
AGGCGCGCT GGTACTGCAA GGAGTGTGCA GAGAGCGTAA CGCCTGGG AAGGAGTAC 1560
ATAACGATGA CCATCAAGGA GATAGAGGAA AAGTACGGCT TTAAGGTAAT CTACAGCGAC 1620
ACCGACGGAT TTTTGGCCAC AATACCTGGA GCCGATGCTG AAACCGTCAA AAAGAAGGCT 1680

GACATTGAAA CTCTCTACCA TGAGGGCGAG GAGTTCGCCG AGGGGCCAAT CCTTATGATA 480
AGCTACGCCG ACGAGGAAGG GGCCAGGGTG ATAACTTGGA AGAACGTGGA TCTCCCCTAC 540
GTTGACGTCG TCTCGACGGA GAGGGAGATG ATAAAGCGCT TCCTCCGTGT TGTGAAGGAG 600
AAAGACCCCG ACGTTCTCAT AACCTACAAC GCGACAACCT TCGACTTCGC CTATCTGAAA 660
AAGCGCTGTG AAAAGCTCGG AATAAACTTC GCCCTCGAA GGGATGGAAG CGAGCCGAAG 720
ATTGAGAGGA TGGGCGACAG GTTTGCCGTC GAAGTGAAGG GACGGATACA CTTGATCTC 780
TATCCTGTGA TAAGACGGAC GATAAACCTG CCCACATACA CGCTTGAGGC CGTTTATGAA 840
GCCGTCTTCG GTCAGCCGAA GGAGAAAGTT TACGCTGAGG AAATAACCAC AGCCTGGGAA 900
ACCGGCGAGA ACCTTGAGAG AGTCGCCCGC TACTCGATGG AAGATGCGAA GGTACATAC 960
GAGCTTGGGA AGGAGTTCCT TCCGATGGAG GCCCAGCTTT CTCGCTTAAT CGGCCAGTCC 1020
CTCTGGGACG TCTCCCGCTC CAGCACTGGC AACCTCGTTG AGTGGTTCCT CCTCAGGAAG 1080
GCCATAGAGA GGAATGAGCT GGCCCCGAAC AAGCCCGATG AAAAGGAGCT GGCCAGAAGA 1140
CGGCAGAGCT ATGAAGGAGG CTATGTAAAA GAGCCCGAGA GAGGGTTGTG GGAGAACATA 1200
GTGTACCTAG ATTTTAGATC CCTGTACCCC TCAATCATCA TCACCCACAA CGTCTCGCCG 1260
GATACGCTCA ACAGAGAAGG ATGCAAGGAA TATGACGTTG CCCACAGGT CGGCCACCGC 1320
TTCTGCAAGG ACTTCCCAGG ATTTATCCCG AGCCTGCTTG GAGACCTCCT AGAGGAGAGG 1380
CAGAAGATAA AGAAGAAGAT GAAGGCCACG ATTGACCCGA TCGAGAGGAA GCTCCTCGAT 1440
TACAGGCAGA GGGCCATCAA GATCCTGGCA AACAGCTACT ACGTTACTA CGGCTATGCA 1500
AGGGCGCGCT GGTA CTGCAA GGAGTGTGCA GAGAGCGTAA CGGCCTGGGG AAGGGAGTAC 1560
ATAACGATGA CCATCAAGGA GATAGAGGAA AAGTACGGCT TTAAGGTAAT CTACAGCGAC 1620
ACCGACGGAT TTTTGGCCAC AATACCTGGA GCCGATGCTG AAACCGTCAA AAAGAAGGCT 1680
ATGGAGTTCC TCAAGTATAT CAACGCCAAA CTTCGGGGCG CGCTTGAGCT CGAGTACGAG 1740
GGCTTCTACA AACGCGGCTT CTTTCGTCACG AAGAAGAAGT ATGCGGTGAT AGACGAGGAA 1800
GGCAAGATAA CAACGCGCGG ACTTGAGATT GTGAGGCGTG ACTGGAGCGA GATAGCGAAA 1860
GAGACGCAGG CGAGGGTTCT TGAAGCTTTG CTAAAGGACG GTGACGTCGA GAAGGCCGTG 1920
AGGATAGTCA AAGAAGTTAC CGAAAAGCTG AGCAAGTACG AGGTTCCGCC GGAGAAAGCTG 1980
GTGATCCACG AGCAGATAAC GAGGGATTTA AAGGACTACA AGGCAACCCG TCCCCACGTT 2040
GCCGTTGCCA AGAGTTGGC CGCGAGAGGA GTCAAAATAC GCCCTGGAAC GGTGATAAGC 2100
TACATCGTGC TCAAGGGCTC TGGGAGGATA GGCGACAGGG CGATACCGTT CGACGAGTTC 2160
GACCCGACGA AGCACAAGTA CGACGCCGAG TACTACATTG AGAACCAGGT TCTCCCAGCC 2220
GTTGAGAGAA TTCTGAGAGC CTTGCGTTAC CGCAAGGAAG ACCTGCGCTA CCAGAAGACG 2280
AGACAGGTTG GTTTGAGTGC TTGGCTGAAG CCGAAGGGAA CT //TAG 2325

Figure 17N

(Hmf-1ike) -Vent DNA POLYMERASE FUSION PROTEIN

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 35)
Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 36)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT	54
GCT CAG AGA GGT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA	108
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA	162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC //	

ATGATACTGG ACACTGATTA CATAACAAAA GATGGCAAGC CTATAATCCG AATTTTAAAG	60
AAAGAGAACG GGGAGTTTAA AATAGAACTT GACCCTCATT TTCAGCCCTA TATATATGCT	120
CTTCTCAAAG ATGACTCCGC TATTGAGGAG ATAAAGGCAA TAAAGGGCGA GAGACATGGA	180
AAAACTGTGA GAGTGCTCGA TGCAGTGAAA GTCAGGAAAA AATTTTGGG AAGGGAAGTT	240
GAAGTCTGGA AGCTCATTTT CGAGCATCCC CAAGACXXXC CAGCTATGCG GGCACAAAATA	300
AGGGAACATC CAGCTGTGGT TGACATTTAC GAATATGACA TACCCTTTGC CAAGCGTTAT	360
CTCATAGACA AGGGCTTGAT TCCCATGGAG GGAGACGAGG AGCTTAAAGCT CCTTGCCCTT	420
GATATTGAAA CGTTTTATCA TGAGGGAGAT GAATTTGGA AGGGCGAGAT AATAATGATT	480
AGTTATGCCG ATGAAGAAGA GGCCAGAGTA ATCACATGGA AAAATATCGA TTTGCCGTAT	540
GTCGATGTTG TGTCCAATGA AAGAGAAATG ATAAAGCGTT TTGTTCAAGT TGTAAAGAA	600
AAAGACCCCG ATGTGATAAT AACTTACAAT GGGACAATT TTGATTTGCC GTATCTCATA	660
AAACGGGCAG AAAAGCTGGG AGTTCGGCTT GTCTTAGGAA GGGACAAAGA ACATCCCGAA	720
CCCAAGATTC AGAGGATGGG TGATAGTTTT GCTGTGAAA TCAAGGGTAG AATCCACTTT	780
GATCTTTTCC CAGTTGTGCG AAGGACGATA AACCTCCCAA CGTATACGCT TGAGGCAGTT	840
TATGAAAGCAG TTTTAGGAAA AACCAAAAGC AAATTAGGAG CAGAGGAAAT TGCCGCTATA	900
TGGGAAACAG AAGAAAGCAT GAAAAAATA GCCCAGTACT CAATGGAAGA TGCTAGGCA	960
ACGTATGAGC TCGGGAAGGA ATTCTTCCCC ATGGAAGCTG AGCTGGCAA GCTGATAGGT	1020
CAAAGTGAT GGGACGTCTC GAGATCAAGC ACCGGCAACC TCGTGGAGTG GTATCTTTTA	1080
AGGTGGCAT ACGCGAGGAA TGAAC TTGCA CCGAACAAC CTGATGAGGA AGAGTATAAA	1140
CGGCGCTTAA GAACAAC TTA CTTGGGAGGA TATGTAAAAG AGCCAGAAAA AGGTTTGTGG	1200
GAAATATCA TTTATTTTGA TTTCCGCAGT CTGTACCCTT CAATAATAGT TACTCACAA	1260
GTATCCCCAG ATACCCCTTGA AAAAGAGGGC TGTAAGAAAT ACGATGTTGC TCCGATAGTA	1320
GGATATAGGT TCTGCAAGGA CTTTCCGGGC TTTATTCCTT CCATACTCGG GGACTTAAT	1380
GCAATGAGGC AAGATATAA GAAGAAAATG AAATCCACAA TTGACCCGAT CGAAAAAGAA	1440
ATGCTCGATT ATAGGCAAAG GGCTATTAAA TTGCTTGCAA ACAGCTATTA CGGCTATATG	1500
GGGTATCCTA AGGCAAGATG GTACTCGAAG GAATGTGCTG AAAGCGTTAC CGCATGGGG	1560
AGACACTACA TAGAGATGAC GATAAGAGAA ATAGAGGAAA AGTTCGGCTT TAAGGTTCTT	1620
TATGCGGACA CTGACGGCTT TTATGCCACA ATACCCGGGG AAAAGCCTGA ACTCATTA	1680
AAGAAAAGCCA AGGAATTCCT AAAC TACATA AACTCCAAAC TTCCAGGTCT GCTTGAGCTT	1740
GAGTATGAGG GCTTTTACTT GAGAGGATTC TTTGTTACAA AAAAGCGCTA TGCAGTCATA	1800
GATGAAGAGG GCAGGATAAC AACAAAGGGC TTGGAAGTAG TAAGGAGAGA TTGGAGTGAG	1860

Replacement Figure

ATAGCTAAGG AGACTCAGGC AAAGGTTTTA GAGGCTATAC TTAAAGAGGG AAGTGTGAA 1920
AAAGCTGTAG AAGTTGTTAG AGATGTTGTA GAGAAATAG CAAAATACAG GGTTCACCTT 1980
GAAAAGCTTG TTATCCATGA GCAGATTACC AGGGATTAA AGGACTACAA AGCCATTGGC 2040
CCTCATGTGG CGATAGCAAA AAGACTTGCC GCAAGAGGGA TAAAAGTGAA ACCGGGCACA 2100
ATAATAAGCT ATATCGTTCT CAAAGGGAGC GGAAGAGATAA GCGATAGGGT AATTTTACTT 2160
ACAGAATACG ATCCTAGAAA ACACAAAGTAC GATCCGGACT ACTACATAGA AAACCAAGTT 2220
TTGCCGGCAG TACTTAGGAT ACTCGAAGCG TTTGGATACA GAAAGGAGGA TTTAAGGTAT 2280
CAAAGCTCAA AACAAACCGG CTTAGATGCA TGGCTCAAGA GGTAG 2325

Figure 170

Vent DNA POLYMERASE - (Hmf-like) FUSION PROTEIN

Nucleotide sequence (SEQ ID NO: 35) // Nucleotide sequence (SEQ ID NO: 63)

Nucleotide sequence (SEQ ID NO: 36) // Nucleotide sequence (SEQ ID NO: 63)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)

V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATACTGG ACACTGATTA CATAACAAA GATGGCAAGC CTATAATCCG AATTTTAAAG 60
AAAGAGAACG GGGAGTTTAA AATAGAACTT GACCTCATT TTCAGCCCTA TATATATGCT 120
CTTCTCAAAG ATGACTCCGC TATTGAGGAG ATAAAGGCAA TAAAGGGCGA GAGACATGGA 180
AAAACGTGA GAGTGCTCGA TGCAGTGA~~AAA~~ AATTTTGGG AAGGGAAGTT 240
GAAGTCTGGA AGCTCATTTT CGAGCATCCC CAAGAC~~XXX~~C CAGCTATGCG GGGCAAAATA 300
AGGGAACATC CAGCTGTGGT TGACATTTAC GAATATGACA TACCCTTTGC CAAGCGTTAT 360
CTCATAGACA AGGGCTTGAT TCCCATGGAG GGAGACGAGG AGCTTAAGCT CCTTGCCTTT 420
GATATTGAAA CGTTTATCA TGAGGGAGAT GAATTTGGAA AGGGCGAGAT AATAATGATT 480
AGTTATGCCG ATGAAGAAGA GGCCAGAGTA ATCACATGGA AAAATATCGA TTTGCCGTAT 540
GTCGATGTTG TGTCCAATGA AAGAGAAATG ATAAAGCGTT TTGTTCAAGT TGTTAAAGAA 600
AAAGACCCCG ATGTGATAAT AACTTACAAT GGGACAATT TTGATTTGCC GTATCTCATA 660
AAACGGGCAG AAAAGCTGGG AGTTCGGCTT GTCTTAGGAA GGGACAAAGA ACATCCCGAA 720
CCCAAGATTC AGAGGATGGG TGATAGTTTT GCTGTGAAA TCAAGGGTAG AATCCACTTT 780
GATCTTTTCC CAGTTGTGCG AAGGACGATA AACCTCCCAA CGTATACGCT TGAGGCAGTT 840
TATGAAAGCAG TTTTAGGAAA AACCAAAAGC AAATTAGGAG CAGAGGAAAT TGCCGCTATA 900
TGGGAAACAG AAGAAAGCAT GAAAAA~~ACTA~~ GCCCAGTACT CAATGGAAGA TGCTAGGGCA 960
ACGTATGAGC TCGGGAAGGA ATTCTTCCCC ATGGAAGCTG AGCTGGCAA GCTGATAGGT 1020
CAAAGTGAT GGGACGTCTC GAGATCAAGC ACCGGCAACC TCGTGGAGTG GTATCTTTTA 1080
AGGGTGCGAT ACGCGAGGAA TGAACCTGCA CCGAACAAAC CTGATGAGGA AGAGTATAAA 1140
CGGCGCTTAA GAACAACCTTA CTGGGGAGGA TATGTAAAAG AGCCAGAAAA AGGTTTGTGG 1200

GAAATATCA TTTATTTGGA TTTCCGCAGT CTGTACCCTT CAATAATAGT TACTACAAC 1260
GTATCCCCAG ATACCCTTGA AAAAGAGGGC TGTAAGAATT ACGATGTTGC TCCGATAGTA 1320
GGATATAGGT TCTGCAAGGA CTTTCCGGGC TTTATTCCTT CCATACTCGG GGACTTAATT 1380
GCAATGAGGC AAGATATAAA GAAGAAAATG AAATCCACAA TTGACCCGAT CGAAAAAGAA 1440
ATGCTCGATT ATAGGCAAAG GGCTATTAAA TTGCTTGCAA ACAGCTATTA CGGCTATATG 1500
GGGTATCCTA AGGCAAGATG GTACTCGAAG GAATGTGCTG AAAGCGTTAC CGCATGGGG 1560
AGACACTACA TAGAGATGAC GATAAGAGAA ATAGAGGAAA AGTTCGGCTT TAAGGTTCTT 1620
TATGCGGACA CTGACGGCTT TTATGCCACA ATACCCGGGG AAAAGCCTGA ACTCATTAAA 1680
AAGAAAGCCA AGGAATTCCT AACTACATA AACTCCAAAC TTCCAGGTCT GCTTGAGCTT 1740
GAGTATGAGG GCTTTTACTT GAGAGGATTC TTTGTTACAA AAAAGCGCTA TGCAGTCATA 1800
GATGAAGAGG GCAGGATAAC AACAAAGGGC TTGGAAGTAG TAAAGGAGAGA TTGGAGTGAG 1860
ATAGCTAAGG AGACTCAGGC AAAGGTTTTA GAGGCTATAC TTAAAAGAGG AAGTGTTGAA 1920
AAAGCTGTAG AAGTTGTTAG AGATGTTGTA GAGAAAATAG CAAAATACAG GGTTCACCTT 1980
GAAAAGCTTG TTATCCATGA GCAGATTACC AGGGATTTAA AGGACTACAA AGCCATTGGC 2040
CCTCATGTG CGATAGCAAA AAGACTTGCC GCAAGAGGA TAAAAGTGAA ACCGGGCACA 2100
ATAATAAGCT ATATCGTTCT CAAAGGGAGC GGAAGATAA GCGATAGGGT AATTTTACTT 2160
ACAGAAATACG ATCCTAGAAA ACACAAGTAC GATCCGGACT ACTACATAGA AAACCAAGTT 2220
TTGCCGGCAG TACTTAGGAT ACTCGAAGCG TTTGGATACA GAAAGGAGGA TTTAAGGTAT 2280
CAAAGCTCAA AACAAACCGG CTTAGATGCA TGGCTCAAGA GG 2325 //

ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA

Figure 17P

Deep Vent- (Hmf-like) DNA polymerase fusion protein

Nucleotide sequence (SEQ ID NO: 37) // Nucleotide sequence (SEQ ID NO: 63)

Nucleotide sequence (SEQ ID NO: 38) // Nucleotide sequence (SEQ ID NO: 63)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
ATGATACTTG ACGCTGACTA CATCACCAGG GATGGGAAGC CGATTATAAG GATTTCAAG 60
AAAGAAAACG GCGAGTTTAA GTTGAGTAC GACAGAAACT TTAGACCTTA CATTACGCT 120
CTCCTCAAAG ATGACTCGCA GATTGATGAG GTTAGGAAGA TAACCGCCGA GAGCATGGG 180
AAGATAGTGA GAATTATAGA TGCCGAAAAG GTAAGGAAGA AGTTCCTGGG GAGCCGATT 240
GAGGTATGGA GGCTGTACTT TGAACACCCT CAGGACXXXC CCGCAATAAG GGATAAGATA 300
AGAGAGCATT CCGCAGTTAT TGACATCTTT GAGTACGACA TTCCGTTCCG GAAGAGGTAC 360

CTAATAGACA	AAGGCCTAAT	TCCAATGGAA	GGCGATGAAG	AGCTCAAGTT	GCTCGCATTT	420
GACATAGAAA	CCCTCTATCA	CGAAGGGGAG	GAGTTCGCGA	AGGGCCCAT	TATAATGATA	480
AGCTATGCTG	ATGAGGAAGA	AGCCAAAGTC	ATAACGTGGA	AAAAGATCGA	TCTCCCGTAC	540
GTCGAGGTAG	TTTCCAGCGA	GAGGGAGATG	ATAAAGCGGT	TCCTCAAGGT	GATAAGGGAG	600
AAAGATCCCG	ATGTTATAAT	TACCTACAAC	GGCGATTCTT	TCGACCTTCC	CTATCTAGTT	660
AAGAGGCCCG	AAAAGCTCGG	GATAAAGCTA	CCCCTGGGAA	GGACGGTAG	TGAGCCAAAG	720
ATGCAGAGGC	TTGGGGATAT	GACAGCGGTG	GAGATAAAGG	GAAGGATACA	CTTTGACCCTC	780
TACCACGTGA	TTAGGAGAAC	GATAAACCTC	CCAACATACA	CCCTCGAGGC	AGTTTATGAG	840
GCAATCTTCG	GAAAGCCAAA	GGAGAAAAGTT	TACGCTCACG	AGATAGCTGA	GGCCTGGGAG	900
ACTGGAAAGG	GACTGGAGAG	AGTTGCAAAAG	TATTCAATGG	AGGATGCAAA	GGTAACGTAC	960
GAGCTCGGTA	GGGAGTTCTT	CCCAATGGAG	GCCCAGCTTT	CAAGGTTAGT	CGGCCAGCCC	1020
CTGTGGGATG	TTTCTAGGTC	TTCAACTGGC	AACTTGGTGG	AGTGGTACCT	CCTCAGGAAG	1080
GCCTACGAGA	GGAATGAATT	GGCTCCAAAC	AAGCCGGATG	AGAGGGAGTA	CGAGAGAAAG	1140
CTAAGGGAGA	GCTACGCTGG	GGGATACGTT	AAGGAGCCGG	AGAAAAGGGCT	CTGGGAGGGG	1200
TTAGTTTCCC	TAGATTTTCAG	GAGCCTGTAC	CCCTCGATAA	TAATCACCCA	TAACGTCTCA	1260
CCGGATACGC	TGAACAGGGA	AGGGTGTAGG	GAATACGATG	TCGCCCCAGA	GGTTGGGCAC	1320
AAGTTCTGCA	AGGACTTCCC	GGGGTTTATC	CCCAGCCTGC	TCAAGAGGTT	ATTGGATGAA	1380
AGGCAAGAAA	TAAAAAGGAA	GATGAAAAGCT	TCTAAAGACC	CAATCGAGAA	GAAGATGCTT	1440
GATTACAGGC	AACGGGCAAT	CAAAATCCTG	GCAAAACAGCT	ATTATGGGTA	TTATGGGTAC	1500
GCAAAAAGCCC	GTTGGTACTG	TAAGGAGTGC	GCAGAGAGCG	TTACGGCCTG	GGGGAGGGAA	1560
TATATAGAGT	TCGTAAGGAA	GGAAGTGGAG	GAAAAGTTCG	GGTTCAAAGT	CTTATACATA	1620
GACACAGATG	GACTCTACGC	CACAATTCTT	GGGGCAAAAC	CCGAGGAGAT	AAAGAAAGAAA	1680
GCCCTAGAGT	TCGTAGATTA	TATAAACGCC	AAGCTCCCAG	GGCTGTTGGA	GCTTGAGTAC	1740
GAGGGCTTCT	ACGTGAGAGG	GTTCTTTCGTG	ACGAAGAAGA	AGTATGCGTT	GATAGATGAG	1800
GAAGGGGAAGA	TAATCACTAG	GGGGCTTGAA	ATAGTCAGGA	GGGACTGGAG	CGAAATAGCC	1860
AAAGAAACCC	AAGCAAAAGT	CCTAGAGGCT	ATCCTAAAGC	ATGGCAACGT	TGAGGGAGGCA	1920
GTAAAGATAG	TTAAGGAGGT	AACTGAAAAG	CTGAGCAAGT	ACGAAATACC	TCCAGAAAAG	1980
CTAGTTATTT	ACGAGCAGAT	CACGAGGCC	CTTCACGAGT	ACAAGGCTAT	AGGTCCGCAC	2040
GTTGCCGTGG	CAAAAAGGTT	AGCCGCTAGA	GGAGTAAAGG	TGAGGCCCTGG	CATGGTGATA	2100
GGGTACATAG	TGCTGAGGGG	AGACGGGCCA	ATAAGCAAGA	GGGCTATCCT	TGCAGAGGAG	2160
TTCGATCTCA	GGAAGCATAA	GTATGACGCT	GAGTATTACA	TAGAAAATCA	GGTTTTACCT	2220
GCCGTTCTTA	GAATATTAGA	GGCCTTTGGG	TACAGGAAAG	AAGACCTCAG	GTGGCAGAAAG	2280
ACTAAACAGA	CAGGTCTTAC	GGCATGGCTT	AACATCAAGA	AGAAG //		2328

ATG	ATG	GGA	GAA	TTA	CCA	ATT	GCC	CCA	GTT	GAC	AGA	CTT	ATA	AGA	AAG	GCT	GGT	54
GCT	CAG	AGA	GTT	AGC	GAG	CAA	GCA	GCT	AAG	GTA	CTT	GCA	GAG	CAC	CTT	GAG	GAA	108
AAA	GCT	ATT	GAG	ATC	GCA	AAA	AAG	GCA	GTA	GAT	CTT	GCA	AAG	CAC	GCA	GGT	AGA	162
AAG	ACC	GTT	AAG	GTC	GAA	GAC	ATT	AAG	CTC	GCA	ATT	AAG	AGC	TGA				

Figure 17Q

Replacement Figure

(Hmflike) - Deep Vent DNA polymerase fusion protein

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 37)
Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 38)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA

ATGATACTTG ACGCTGACTA CATCACCGAG GATGGGAAGC CGATTATAAG GATTTCAAG 60
AAAGAAAACG GCGAGTTTAA GGTGAGTAC GACAGAAACT TTAGACCTTA CATTTACGCT 120
CTCCTCAAAG ATGACTCGCA GATTGATGAG GTTAGGAAGA TAACCGCCGA GAGCATGGG 180
AAGATAGTGA GAATTATAGA TGCCGAAAAG GTAAGGAAGA AGTTCCTGGG GAGGCCGATT 240
GAGGTATGGA GGCTGTACTT TGAACACCCCT CAGGACXXXC CCGCAATAAG GGATAAGATA 300
AGAGAGCAAT CCGCAGTTAT TGACATCTTT GAGTACGACA TTCCGTTCCG GAAGAGGTAC 360
CTAATAGACA AAGGCCTAAT TCCAATGGAA GGCGATGAAG AGCTCAAGTT GCTCGCATTT 420
GACATAGAAA CCTCTATCA CGAAGGGGAG GAGTTCGCGA AGGGGCCCAT TATAATGATA 480
AGCTATGCTG ATGAGGAAGA AGCCAAAGTC ATAACGTGGA AAAAGATCGA TCTCCCGTAC 540
GTCGAGGTAG TTTCCAGCGA GAGGGAGATG ATAAAGCGGT TCCTCAAGGT GATAAGGGAG 600
AAAGATCCCG ATGTTATAAT TACCTACAAC GCGGATTCTT TCGACCTTCC CTATCTAGTT 660
AAGAGGGCCG AAAAGCTCGG GATAAAGCTA CCCCTGGGAA GGGACGGTAG TGAGCCAAAG 720
ATGCAGAGGC TTGGGGATAT GACAGCGGTG GAGATAAAGG GAAGGATACA CTTTGACCTC 780
TACCACGTGA TTAGGAGAAC GATAAACCTC CCAACATACA CCCTCGAGGC AGTTTATGAG 840
GCAATCTTCG GAAAGCCAAA GGAGAAAGTT TACGCTCACG AGATAGCTGA GGCCTGGGAG 900
ACTGGAAGG GACTGGAGAG AGTTGCAAAG TATTCAATGG AGGATGCAA GGTAAACGTAC 960
GAGCTCGGTA GGGAGTTCTT CCCAATGGAG GCCCAGCTTT CAAGGTTAGT CGGCCAGCCC 1020
CTGTGGGATG TTTCTAGGTC TTCAACTGGC AACTTGGTGG AGTGGTACCT CCTCAGGAAG 1080
GCCTACGAGA GGAATGAATT GGCTCCAAAC AAGCCGGATG AGAGGGAGTA CGAGAGAAAGG 1140
CTAAGGGAGA GCTACGCTGG GGGATACGTT AAGGAGCCGG AGAAAGGGCT CTGGGAGGGG 1200
TTAGTTTCCC TAGATTTTCAG GAGCCTGTAC CCCTCGATAA TAATCACCCA TAACGTCTCA 1260
CCGGATACGC TGAACAGGGA AGGGTGTAGG GAATACGATG TCGCCCCAGA GGTGGGCAC 1320
AAGTTCTGCA AGGACTTCCC GGGTTTATC CCCAGCCTGC TCAAGAGGTT ATTGGATGAA 1380
AGGCAAGAAA TAAAAGGAA GATGAAAGCT TCTAAAGACC CAATCGAGAA GAAGATGCTT 1440
GATTACAGGC AACGGGCAAT CAAAATCCTG GCAAACAGCT ATTATGGGTA TTATGGGTAC 1500
GCAAAAGCCC GTTGTACTG TAAGGAGTGC GCAGAGAGCG TTACGGCCTG GGGAGGGAA 1560

TATATAGAGT	TCGTAAGGAA	GGAAGTTGGAG	GAAAAGTTTCG	GGTTCAAAGT	CTTATACATA	1620
GACACAGATG	GAAGTTACGC	CACAATTCCT	GGGCAAAAC	CCGAGGAGAT	AAAGAAGAAA	1680
GCCCTAGAGT	TCGTAGATTA	TATAAACGCC	AAGTCCAG	GGCTGTTGGA	GCTTGAGTAC	1740
GAGGGCTTCT	ACGTGAGAGG	GTTCTTCGTG	ACGAAGAAGA	AGTATGCCGT	GATAGATGAG	1800
GAAGGGAAGA	TAATCACTAG	GGGCTTGAA	ATAGTCAGGA	GGGACTGGAG	CGAAATAGCC	1860
AAAGAAACCC	AAGCAAAAGT	CCTAGAGGCT	ATCCTAAAGC	ATGGCAACGT	TGAGGAGGCA	1920
GTAAGAGATAG	TAAAGGAGGT	AAGTGAAG	CTGAGCAAGT	ACGAAATACC	TCCAGAAAG	1980
CTAGTTATTT	ACGAGCAGAT	CACGAGGCC	CTTCACGAGT	ACAAGGCTAT	AGTCCGCAC	2040
GTTGCCGTGG	CAAAAAGTT	AGCCGCTAGA	GGAGTAAAGG	TGAGGCCCTGG	CATGGTGATA	2100
GGGTACATAG	TGCTGAGGG	AGACGGCCA	ATAAGCAAGA	GGCTATCCT	TGCAGAGGAG	2160
TTCGATCTCA	GGAAGCATAA	GTATGACGCT	GAGTATTACA	TAGAAAATCA	GGTTTTACCT	2220
GCCGTTCTTA	GAATATTAGA	GGCCTTTGGG	TACAGGAAAG	AAGACCTCAG	GTGGCAGAAAG	2280
ACTAAACAGA	CAGGTCTTAC	GGCATGGCTT	AACATCAAGA	AGAAG TAA		2328

Figure 17R

JDF-3 - (Hmf-like) fusion protein

Nucleotide sequence (SEQ ID NO: 39) // Nucleotide sequence (SEQ ID NO: 63)
Nucleotide sequence (SEQ ID NO: 40) // Nucleotide sequence (SEQ ID NO: 63)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATCCTTGACGTTGATTACATCACCGAGAAATGAAAGCCCGTCAATCAGGGTCTTCAAGAAAGAGAACGGCGAGTTCAGGATTGAATACGACCGGAGTTCGAGCCCTACTTCT
ACGCGCTCCTCAGGGACGACTCTGCCATCGAAGAAATCAAAAAGATAAACCGCGGAGAGGCACGGCAGGGTCGTTAAGTTAAGCGCGGAGAGAGTGAAGAAAAGTTCCCTCGG
CAGGTCTGTGGAGGTCGTGGTCTCTACTTACGACCCGACGACXXXCCGGCAATCCCGACAAATAAGGAAGCACCCCGGGTCAATCGACATCGAGTACGACATACCC
TTCGCCAAGCGCTACCTCATAGACAAGGGCCTAATCCCGATGGAAAGGTGAGGAAGAGCTTAAACTCATGTCTTCGACATCGAGACGCTTACACGAGGGAGAGAGTTTGAA
CCGGCCGATTCTGATGATAAGCTACGCCGATGAAAGCGAGCGCGGTGATAACCTGGAAGAAGATCGACCTTCTTACGTTGAGGTTGTCTCCACCGAGAAAGGAGATGATTAA
GCGCTTCTTGAGGTCGTTAAGGAGAGAGACCCGACGTCGTGATAACATAACGGCGACAACTTCGACTTCGCTACCTGAAAAGCGCTGTGAGAAAGCTTGCGTGAGCTTT
ACCTCGGAGGACGGGAGCGGAGCGAAGATACAGCGCATGGGGACAGGTTTGCGGTGAGGTGAAGGCGAGGTACACTTCGACCTTTATCCAGTCAATAAGGCGCACCATAA
ACCTCCGACCTACACCTTGAGGCTGTATACGAGCGGTTTTCGGCAAGCCCAAGGAGAGGTCTACGCCGAGGAGATAGCCACCGCTGGGAGACCGGCGAGGGCTTGAGAG
GGTCGCGCGCTACTCGATGGAGGACGCGAGGTTACCTACGAGCTTGCGAGGAGTTCTTCCGATGGAGGCCAGCTTTCAGGCTCATCGGCCAAGGCTCTGGGACGTTTCC
CGCTCCAGCACCGGCAACCTCGTCGAGTGGTTCTCCTAAGGAAGGCTACGAGAGGAACGAACTCGCTCCCAACAAAGCCGACGAGAGGAGCTGGCGAGGAGAAAGGGGGCT
ACGCGGTGGCTACGTCAAGGAGCCGGAGCGGGACTGTGGGACAAATATCGTGTATCTAGACTTTCGTAAGTCTTACCTTCAATCATATAATCACCAACGTCCTCGCAGATAC
GCTCAACCGGAGGGGTAGGAGCTACGACGTTGCCCGGAGTCGGTCACAAGTTCTGCAAGGACTTCCCGGCTTCAATCCGAGCTTCGCAACCGCTCGGAAACCTGCTGGAGGAAAGG
CAGAAGATAAAGAGGAAGATGAAGGCAACTCTCGACCCGCTGGAGAAAGATCTCCTCGATTACAGGCAACGGCTATCAAGATTCTCGCAACAGCTACTACGGCTACGCGCT
ATGCCAGGGCAAGATGGTACTGCGAGGTGCGCGGAGAGCGTTACGGCATGGGGAAGGGAGTACATCGAAATGGTCAATCAGAGAGCTTGAGGAAAGTTTCGGTTTAAAGTCCT
CTATGCAGACACAGCGGTCTCCATGCCACCATTCCTGGAGCGGACGCTGAACAGTCAAGAAAAGGCAATGGAGTTCTTAAACTATATCAATCCCAAACCTGCCCGCTTCTC
GAACTCGAATACGAGGGCTTCTACGTCAAGGGGCTTCTTCGTCAAGAAAGTAACGCGGTCAATCGACGAGGAGGCAAGATAACACGCGGGCTTGAGATAGTCAGGCGG

ACTGGAGCGAGATAGCGAAGGAGACGCGAGCGAGGGTTTTTGGAGGCGGATACCTAGGCACGGTGACGTTGAAGAGGCCGTGAGAAATTGTCAAGGAAGTCAACCGAAAAGCTGAGCAA
GTACGAGGTTCCGCCGGAGAAGCTGGTTATCCACGAGCAGATAACGCGGAGCTCAAGGACTACAAGGCCACCGGCCACCGCATAGCCATAGCGAAGcGTTTGCCCGCCAGAGGT
GTTAAATCCGGCCCGAACTGTGATAAAGCTACATCGTTCTGAAGGCTCCGAAAGGATAGGCCAGAGGCGGATTCCCTTCGACGAGTTTCGACCCGACGAAAGCACAAAGTACGATG
CGGACTACTACATCGAGAACCAGGTTCTGCCGGCAGTTGAGAGAATCCTCAGGGCCTTCGGCTACCGCAAGGAAGACCTGCGCTACCAAGAAGACGAGGCAGGTCGGGCTTGCGCGC
GTGGCTGAAGCCGAAGGGGAAGAAG//

ATG	ATG	GGA	GAA	TTA	CCA	ATT	GCC	CCA	GTT	GAC	AGA	CTT	ATA	AGA	AAG	GCT	GGT	54
GCT	CAG	AGA	GTT	AGC	GAG	CAA	GCA	GCT	AAG	GTA	CTT	GCA	GAG	CAC	CTT	GAG	GAA	108
AAA	GCT	ATT	GAG	ATC	GCA	AAA	AAG	GCA	GTA	GAT	CTT	GCA	AAG	CAC	GCA	GGT	AGA	162
AAG	ACC	GTT	AAG	GTC	GAA	GAC	ATT	AAG	CTC	GCA	ATT	AAG	AGC	TGA				

Figure 17S

(Hmf-like) - JDF-3 fusion protein

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 39)
Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 40)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATG	ATG	GGA	GAA	TTA	CCA	ATT	GCC	CCA	GTT	GAC	AGA	CTT	ATA	AGA	AAG	GCT	GGT	54
GCT	CAG	AGA	GTT	AGC	GAG	CAA	GCA	GCT	AAG	GTA	CTT	GCA	GAG	CAC	CTT	GAG	GAA	108
AAA	GCT	ATT	GAG	ATC	GCA	AAA	AAG	GCA	GTA	GAT	CTT	GCA	AAG	CAC	GCA	GGT	AGA	162
AAG	ACC	GTT	AAG	GTC	GAA	GAC	ATT	AAG	CTC	GCA	ATT	AAG	AGC	//				

ATGATCCTTGACGTTGATTACATCACCGAGAATGGAAGCCCGTCATCAGGGTCTTCAAGAAGGAGAAACGGCGAGTTCAGGATTGAATACGACCGCGAGTTCGAGCC
CTACTTCTACGCGTCTCCTCAGGGACGACTCTGCCATCGAAGAAATCAAAAGATAACCGGGAGAGGCACGGCAGGGTCGTTAAGGTTAAGCGCGCGAGAAAGTGTA
AGAAAAGTTCCTCGGCAGGTCGTGGAGGTCGTGGTCTCTACTTCACGCACCCGCGAGGACXXXCCGGCAATCCCGCACAAAATAAGGAAGCACCCCGCGGTCATC
GACATCTACGAGTACGACATACCCCTTCGCCAAGCGCTACCTCATAGACAAGGCCCTAATCCCGATGGAAGGTGAGGAAGAGCTTAAACTCATGTCCTTGAQATCGA
GACGCTCTACACGAGGAGAAAGAGTTTGGAAACCGGCCGATTCTGATGATAAGCTACGCCGATGAAGCGAGGCGCGTGATAAACCTGGAAGAAGATCGACCTTC
CTTACGTTGAGGTTGTCTCCACCGAGAAGGAGATGATTAAAGCGTTCTTGAGGGTCGTTAAGGAGAAAGGACCCGGACCGTGCTGATACATACAACGGCGACAACCTTC
GACTTCGCCCTACCTGAAAAGCGCTGTGAGAAGCTTGCGGTGAGCTTTACCCCTCGGAGGACGGGAGCGAGCCGAAGATACAGCGCATGGGGACAGGTTTGCGGT
CGAGGTGAAGGCAGGGTACACTTCGACCTTTATCCAGTCATAAGCGCACCAATAAACCTCCGACCTACACCCCTTGAGGCTGTATACGAGCGGTTTTCGGCAAGC
CCAAGGAGAAGGCTACGCCGAGGAGATAGCCACCGCTGGAGACCGCGAGGGCTTGAGAGGGTCGCGCGCTACTCGATGGAGGACGCGAGGTTACCTACGAG
CTTGGCAGGAGTTCTTCCCGATGGAGGCCCAGCTTTTCAGGCTCATCGGCCAAGCCCTCTGGGACGTTTCCCGCTCCAGCACCGCAACCTCGTCGAGTGGTTCCT
CCTAAGGAAGGCTACGAGAGGAACGAATCGCTCCCAACAGCCGACGAGAGGGGCTACGcCGGTGGCTACGTCAAGGAGCCGG
AGCGGGACTGTGGGACAAATATCGTGATCTAGACTTTCGTAGTCTCTACCTTCAATCAATCACCCACACAGTCTCGCCAGATACGCTCAACCGCGAGGGGTGT
AGGAGCTACGACGTTGCCCGGAGGTCGGTCAAAAGTTCTGTCAAGGACTTCCCCGGCTTCATTCGAGCCCTGCTCGGAAACCTGCTGGAGGAAAGCGCAGAGATAAA

GAGGAAGATGAAGGCAACTCTCGACCCGCTGGAGAAGAAATCTCCTCGATTACAGGCAACGGC**GC**ATCAAGATTCTCGCCAACAGCTACTACGGCTACTACGGCTATG
CCAGGGCAAGATGGTACTGTCAGGGAGTGCGCCGAGAGCGTTACGGCATGGGGAAGGGAGTACATCGAAATGGTCAATCAGAGAGCTTGAGGAAAAAGTTTCGGTTTTAAA
GTCCCTCTATGCAGACACAGACGGTCTCCATGCCACCAATTCCTGGAGCGGACGCTGAACAGTCAAGAAAAAAGGCAATGGAGTTCTTAAACTATATCAATCCCAAACT
GCCCCGCCCTTCTCGAACTCGAATACGAGGGCTTCTACGTCAGGGGCTTCTTCGTCAAGAAAGTAACGCGGTCAATCGACGAGGGCAAGATAACCAACGCGCG
GGCTTGAGATAGTCAGGCGGACTGGAGCGAGATAGCGAAAGGAGACGCGAGGGTTTGGAGCGGATACTCAGGCACGGTGACGTTGAAGAGGCCGTCAGAAATT
GTCAGGGAGTCAACCGAAAAGCTGAGCAAGTACGAGGTTCCGCCGGAGAAGCTGGTTATCCACGAGCAGATAACGCGCGAGCTCAAGGACTACAAGGCCACCGGCCC
GCACGTAGCCATAGCGAAGcGTTTGGCCGCCAGAGGTGTTAAATCCGGCCCGAACTGTGATAAGCTACATCGTTCTGAAGGCTCCGGAAGGATAGGCGACAGGG
CGATTCCCTTCGACGAGTTTCGACCCGACGAAGCACAAAGTACGATGCGGACTACTACATCGAGAACCAAGTTCTGCCCCGCGAGTTGAGAGAAATCCTCAGGGCCTTCGGC
TACCGCAAGGAAGACCTGCGCTACCAGAAGACGAGGCAGGTCGGGCTTGGCGCGTGGCTGA

Replacement Figure

Figure 17T

Pyrococcus furiosus DSM 3638, Archaeal hostone (HMF-1) section 85 of 173 of the complete genome.
ACCESSION No: AE010210 REGION: complement (8333..9082)
/product="pcna sliding clamp (proliferating-cell nuclear antigen) "

Nucleotide sequence (SEQ ID NO: 67)

Amino acid sequence (SEQ ID NO: 68)

M	P	F	E	I	V	F	E	G	A	K	E	F	A	Q	L	I	D	18
ATG	CCA	TTT	GAA	ATC	GTA	TTT	GAA	GGT	GCA	AAA	GAG	TTT	GCC	CAA	CTT	ATA	GAC	54
T	A	S	K	L	I	D	E	A	A	F	K	V	T	E	D	G	I	36
ACC	GCA	AGT	AAG	TTA	ATA	GAT	GAG	GCC	GCG	TTT	AAA	GTT	ACA	GAA	GAT	GGG	ATA	108
S	M	R	A	M	D	P	S	R	V	V	L	I	D	L	N	L	P	54
AGC	ATG	AGG	GCC	ATG	GAT	CCA	AGT	AGA	GTT	GTC	CTG	ATT	GAC	CTA	AAT	CTC	CCG	162
S	S	I	F	S	K	Y	E	V	V	E	P	E	T	I	G	V	N	72
TCA	AGC	ATA	TTT	AGC	AAA	TAT	GAA	GTT	GTT	GAA	CCA	GAA	ACA	ATT	GGA	GTT	AAC	216
M	D	H	L	K	K	I	L	K	R	G	K	A	K	D	T	L	I	90
ATG	GAC	CAC	CTA	AAG	AAG	ATC	CTA	AAG	AGA	GGT	AAA	GCA	AAG	GAC	ACC	TTA	ATA	270
L	K	K	G	E	E	N	F	L	E	I	T	I	Q	G	T	A	T	108
CTC	AAG	AAA	GGA	GAG	GAA	AAC	TTC	TTA	GAG	ATA	ACA	ATT	CAA	GGA	ACT	GCA	ACA	324
R	T	F	R	V	P	L	I	D	V	E	E	M	E	V	D	L	P	126
AGA	ACA	TTT	AGA	GTT	CCC	CTA	ATA	GAT	GTA	GAA	GAG	ATG	GAA	GTT	GAC	CTC	CCA	378
E	L	P	F	T	A	K	V	V	V	L	G	E	V	L	K	D	A	144
GAA	CTT	CCA	TTC	ACT	GCA	AAG	GTT	GTA	GTT	GGA	GAA	GTC	CTA	AAA	GAT	GCT		432
V	K	D	A	S	L	V	S	D	S	I	K	F	I	A	R	E	N	162

Replacement

Figure

GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT	486
E F I M K A E G E T Q E V E I K L T	180
GAA TTT ATA ATG AAG GCA GAG GGA GAA ACC CAG GAA GTT GAG ATA AAG CTA ACT	540
L E D E G L L D I E V Q E E T K S A	198
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA	594
Y G V S Y L S D M V K G L G K A D E	216
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA	648
V T I K F G N E M P M Q M E Y Y I R	234
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA	702
D E G R L T F L L A P R V E E *	250
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG TGA	750

Figure 17U

(PCNA)-Taq DNA polymerase fusion protein

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 65)

Amino acid sequence (SEQ ID NO: 68) // Amino acid sequence (SEQ ID NO: 66)

M P F E I V F E G A K E F A Q L I D	18
ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC	54
T A S K L I D E A A F K V T E D G I	36
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA	108
S M R A M D P S R V V L I D L N L P	54
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG	162

Replacement

Figure

S	S	I	F	S	K	Y	E	V	V	E	P	E	T	I	G	V	N	72
TCA	AGC	ATA	TTT	AGC	AAA	TAT	GAA	GTT	GTT	GAA	CCA	GAA	ACA	ATT	GGA	GTT	AAC	216
M	D	H	L	K	K	I	L	K	R	G	K	A	K	D	T	L	I	90
ATG	GAC	CAC	CTA	AAG	AAG	ATC	CTA	AAG	AGA	GGT	AAA	GCA	AAG	GAC	ACC	TTA	ATA	270
L	K	K	G	E	E	N	F	L	E	I	T	I	Q	G	T	A	T	108
CTC	AAG	AAA	GGA	GAG	GAA	AAC	TTC	TTA	GAG	ATA	ACA	ATT	CAA	GGA	ACT	GCA	ACA	324
R	T	F	R	V	P	L	I	D	V	E	E	M	E	V	D	L	P	126
AGA	ACA	TTT	AGA	GTT	CCC	CTA	ATA	GAT	GTA	GAA	GAG	ATG	GAA	GTT	GAC	CTC	CCA	378
E	L	P	F	T	A	K	V	V	V	L	G	E	V	L	K	D	A	144
GAA	CTT	CCA	TTC	ACT	GCA	AAG	GTT	GTA	GTT	CTT	GGA	GAA	GTC	CTA	AAA	GAT	GCT	432
V	K	D	A	S	L	V	S	D	S	I	K	F	I	A	R	E	N	162
GTT	AAA	GAT	GCC	TCT	CTA	GTG	AGT	GAC	AGC	ATA	AAA	TTT	ATT	GCC	AGG	GAA	AAT	486
E	F	I	M	K	A	E	G	E	T	Q	E	V	E	I	K	L	T	180
GAA	TTT	ATA	ATG	AAG	GCA	GAG	GGA	GAA	ACC	CAG	GAA	GTT	GAG	ATA	AAG	CTA	ACT	540
L	E	D	E	G	L	L	D	I	E	V	Q	E	E	T	K	S	A	198
CTT	GAA	GAT	GAG	GGA	TTA	TTG	GAC	ATC	GAG	GTT	CAA	GAG	GAG	ACA	AAG	AGC	GCA	594
Y	G	V	S	Y	L	S	D	M	V	K	G	L	G	K	A	D	E	216
TAT	GGA	GTC	AGC	TAT	CTC	TCC	GAC	ATG	GTT	AAA	GGA	CTT	GGA	AAG	GCC	GAT	GAA	648
V	T	I	K	F	G	N	E	M	P	M	Q	M	E	Y	Y	I	R	234
GTT	ACA	ATA	AAG	TTT	GGA	AAT	GAA	ATG	CCC	ATG	CAA	ATG	GAG	TAT	TAC	ATT	AGA	702
D	E	G	R	L	T	F	L	L	A	P	R	V	E	E				250
GAT	GAA	GGA	AGA	CTT	ACA	TTC	CTA	CTG	GCT	CCA	AGA	GTT	GAA	GAG				
		G	G	G														
		//	GGC	GGC	GGT													
V	T	S	G	M	L	P	L	F	E	P	K	G	R	V	L	L	V	

Replacement

Figure

GTC ACT AGT GGG ATG CTG CCC CTC TTT GAG CCC AAG GGC CGG GTC CTC CTG GTG
D G H H L A Y R T F H A L K G L T T
GAC GGC CAC CAC CTG GCC TAC CGC ACC TTC CAC GCC CTG AAG GGC CTC ACC ACC
S R G E P V Q A V Y G F A K S L L K
AGC CGG GGG GAG CCG GTG CAG GCG GTC TAC GGC TTC GCC AAG AGC CTC CTC AAG
A L K E D G D A V I V F D A K A P
GCC CTC AAG GAG GAC GGG GAC GCG GTG ATC GTG GTC TTT GAC GCC AAG GCC CCC
S F R H E A Y G G Y K A G R A P T P
TCC TTC CGC CAC GAG GCC TAC GGG GGG TAC AAG GCG GGC CGG GCC CCC ACG CCA
E D F P R Q L A L I K E L V D L L G
GAG GAC TTT CCC CGG CAA CTC GCC CTC ATC AAG GAG CTG GTG GAC CTC CTG GGG
L A R L E V P G Y E A D D V L A S L
CTG GCG CGC CTC GAG GTC CCG GGC TAC GAG GCG GAC GTC CTG GCC AGC CTG
A K K A E K E G Y E V R I L T A D K
GCC AAG AAG GCG GAA AAG GAG GGC TAC GAG GTC CGC ATC CTC ACC GCC GAC AAA
D L Y Q L L S D R I H V L H P E G Y
GAC CTT TAC CAG CTC CTT TCC GAC CGC ATC CAC GTC CTC CAC CCC GAG GGG TAC
L I T P A W L W E K Y G L R P D Q W
CTC ATC ACC CCG GCC TGG CTT TGG GAA AAG TAC GGC CTG AGG CCC GAC CAG TGG
A D Y R A L T G D E S D N L P G V K
GCC GAC TAC CGG GCC CTG ACC GGG GAC GAG TCC GAC AAC CTT CCC GGG GTC AAG
G I G E K T A R K L L E E W G S L E
GGC ATC GGG GAG AAG ACG GCG AGG AAG CTT CTG GAG GAG TGG GGG AGC CTG GAA
A L L K N L D R L K P A I R E K I L
GCC CTC CTC AAG AAC CTG GAC CGG CTG AAG CCC GCC ATC CGG GAG AAG ATC CTG

Replacement

Figure

A H M D D L L K L S W D L A K V R T D
GCC CAC ATG GAC GAT CTG AAG CTC TCC TGG GAC CTG GCC AAG GTG CGC ACC GAC

L P L E V D F A K R R E P D R E R L
CTG CCC CTG GAG GTG GAC TTC GCC AAA AGG CGG GAG CCC GAC CGG GAG AGG CTT

R A F L E R L E F G S L L H E F G L
AGG GCC TTT CTG GAG AGG CTT GAG TTT GGC AGC CTC CTC CAC GAG TTC GGC CTT

L E S P K A L E E A P W P P E G A
CTG GAA AGC CCC AAG GCC CTG GAG GAG GCC CCC TGG CCC CCG GAA GGG GCC

F V G F V L S R K E P M W A D L L A
TTC GTG GGC TTT GTG CTT TCC CGC AAG GAG CCC ATG TGG GCC GAT CTT CTG GCC

L A A A R G G R V H R A P E P Y K A
CTG GCC GCC GCG AGG GGG GGC CGG GTC CAC CGG GCC CCC GAG CCT TAT AAA GCC

L R D L K E A R G L L A K D L S V L
CTC AGG GAC CTG AAG GAG GCG GGG CTT CTC GCC AAA GAC CTG AGC GTT CTG

A L R E G L G L P P G D D P M L L A
GCC CTG AGG GAA GGC CTT GGC CTC CCG CCC GGC GAC GAC CCC ATG CTC CTC GCC

Y L L D P S N T T P E G V A R R Y G
TAC CTC CTG GAC CCT TCC AAC ACC ACC CCC GAG GGG GTG GCC CGG CGC TAC GGC

G E W T E E A G E R A A L S E R L F
GGG GAG TGG ACG GAG GAG GCG GGG GAG CGG GCC CTT TCC GAG AGG CTC TTC

A N L W G R L E G E E R L L W L Y R
GCC AAC CTG TGG GGG AGG CTT GAG GGG GAG AGG CTC CTT TGG CTT TAC CGG

E V E R P L S A V L A H M E A T G V
GAG GTG GAG AGG CCC CTT TCC GCT GTC CTG GCC CAC ATG GAG GCC ACG GGG GTG

R L D V A Y L R A L S L E V A E E I
CGC CTG GAC GTG GCC TAT CTC AGG GCC TTG TCC CTG GAG GTG GCC GAG GAG ATC

Replacement

Figure

A	R	L	E	A	E	V	F	R	L	A	G	H	P	F	N	L	N
GCC	CGC	CTC	GAG	GCC	GAG	GTC	TTC	CGC	CTG	GCC	GGC	CAC	CCC	TTC	AAC	CTC	AAC
S	R	D	Q	L	E	R	V	L	F	D	E	L	G	L	P	A	I
TCC	CGG	GAC	CAG	CTG	GAA	AGG	GTC	CTC	TTT	GAC	GAG	CTA	GGG	CTT	CCC	GCC	ATC
G	K	T	E	K	T	G	K	R	S	T	S	A	A	V	L	E	A
GGC	AAG	ACG	GAG	AAG	ACC	GGC	AAG	CGC	TCC	ACC	AGC	GCC	GCC	GTC	CTG	GAG	GCC
L	R	E	A	H	P	I	V	E	K	I	L	Q	Y	R	E	L	T
CTC	CGC	GAG	GCC	CAC	CCC	ATC	GTG	GAG	AAG	ATC	CTG	CAG	TAC	CGG	GAG	CTC	ACC
K	L	K	S	T	Y	I	D	P	L	P	D	L	I	H	P	R	T
AAG	CTG	AAG	AGC	ACC	TAC	ATT	GAC	CCC	TTG	CCG	GAC	CTC	ATC	CAC	CCC	AGG	ACG
G	R	L	H	T	R	F	N	Q	T	A	T	A	T	G	R	L	S
GGC	CGC	CTC	CAC	ACC	CGC	TTC	AAC	CAG	ACG	GCC	ACG	GCC	ACG	GGC	AGG	CTA	AGT
S	S	D	P	N	L	Q	N	I	P	V	R	T	P	L	G	Q	R
AGC	TCC	GAT	CCC	AAC	CTC	CAG	AAC	ATC	CCC	GTC	CGC	ACC	CCG	CTT	GGG	CAG	AGG
I	R	R	A	F	I	A	E	E	G	W	L	L	V	A	L	D	Y
ATC	CGC	CGG	GCC	TTC	ATC	GCC	GAG	GAG	GGG	TGG	CTA	TTG	GTG	GCC	CTG	GAC	TAT
S	Q	I	E	L	R	V	L	A	H	L	S	G	D	E	N	L	I
AGC	CAG	ATA	GAG	CTC	AGG	GTG	CTG	GCC	CAC	CTC	TCC	GGC	GAC	GAG	AAC	CTG	ATC
R	V	F	Q	E	G	R	D	I	H	T	E	T	A	S	W	M	F
CGG	GTC	TTC	CAG	GAG	GGG	CGG	GAC	ATC	CAC	ACG	GAG	ACC	GCC	AGC	TGG	ATG	TTC
G	V	P	R	E	A	V	D	P	L	M	R	R	A	A	K	T	I
GGC	GTC	CCC	CGG	GAG	GCC	GTG	GAC	CCC	CTG	ATG	CGC	CGG	GCC	AAG	ACC	ATC	
N	F	G	V	L	Y	G	M	S	A	H	R	L	S	Q	E	L	A
AAC	TTC	GGG	GTC	CTC	TAC	GGC	ATG	TCG	GCC	CAC	CGC	CTC	TCC	CAG	GAG	CTA	GCC
I	P	Y	E	E	A	Q	A	F	I	E	R	Y	F	Q	S	F	P

Replacement

Figure


```

ATC CCT TAC GAG GAG GCC CAG GCC TTC ATT GAG CGC TAC TTT CAG AGC TTC CCC
K   V   R   A   W   I   E   K   T   L   E   E   G   R   R   R   G   Y
AAG GTG CGG GCC TGG ATT GAG AAG ACC CTG GAG GAG GGC AGG AGG CGG GGG TAC
V   E   T   L   F   G   R   R   R   Y   V   P   D   L   E   A   R   V
GTG GAG ACC CTC TTC GGC CGC CGC TAC GTG CCA GAC CTA GAG GCC CGG GTG
K   S   V   R   E   A   A   E   R   M   A   F   N   M   P   V   Q   G
AAG AGC GTG CGG GAG GCG GCC GAG CGC ATG GCC TTC AAC ATG CCC GTC CAG GGC
T   A   A   D   L   M   K   L   A   M   V   K   L   F   P   R   L   E
ACC GCC GCC GAC CTC ATG AAG CTG GCT ATG GTG AAG CTC TTC CCC AGG CTG GAG
E   M   G   A   R   M   L   L   Q   V   H   D   E   L   V   L   E   A
GAA ATG GGG GCC AGG ATG CTC CTT CAG GTC CAC GAC GAG CTG GTC CTC GAG GCC
P   K   E   R   A   E   A   V   A   R   L   A   K   E   V   M   E   G
CCA AAA GAG AGG GCG GAG GCC GTG GCC CGG CTG GCC AAG GAG GTC ATG GAG GGG

V   Y   P   L   A   V   P   L   E   V   E   V   G   I   G   E   D   W
GTG TAT CCC CTG GCC GTG CCC CTG GAG GTG GAG GTG GGG ATA GGG GAG GAC TGG
L   S   A   K   E   G   I   D   G   R   G   G   G   G   H   H   H   H
CTC TCC GCC AAG GAG GGC ATT GAT GGC CGC GGC GGA GGC CAT CAT CAT CAT
H   H   *
CAT CAT TAA

```

Figure 17V

Taq DNA polymerase- (PCNA) fusion protein

Replacement

Figure

Nucleotide sequence (SEQ ID NO: 65) //Nucleotide sequence (SEQ ID NO: 67)
Amino acid sequence (SEQ ID NO: 66) /Amino acid sequence (SEQ ID NO: 68)

G G G
// GGC GGC GGT

V T S G M L P L F E P K G R V L L V
GTC ACT AGT GGG ATG CTG CCC CTC TTT GAG CCC AAG GGC CGG GTC CTC CTG GTG

D G H L A Y R T F H A L K G L T T
GAC GGC CAC CAC CTG GCC TAC CGC ACC TTC CAC GCC CTG AAG GGC CTC ACC ACC

S R G E P V Q A V Y G F A K S L L K
AGC CGG GGG GAG CCG GTG CAG GCG GTC TAC GGC TTC GCC AAG AGC CTC CTC AAG

A L K E D G D A V I V F D A K A P
GCC CTC AAG GAG GAC GGG GAC GCG GTG ATC GTG GTC TTT GAC GCC AAG GCC CCC

S F R H E A Y G G Y K A G R A P T P
TCC TTC CGC CAC GAG GCC TAC GGG GGG TAC AAG GCG GGC CGG GCC CCC ACG CCA

E D F P R Q L A L I K E L V D L L G
GAG GAC TTT CCC CGG CAA CTC GGC CTC ATC AAG GAG CTG GTG GAC CTC CTG GGG

L A R L E V P G Y E A D D V L A S L
CTG GCG CGC CTC GAG GTC CCG GGC TAC GAG GCG GAC GAC GTC CTG GCC AGC CTG

A K K A E K E G Y E V R I L T A D K
GCC AAG AAG GCG GAA AAG GAG GGC TAC GAG GTC CGC ATC CTC ACC GCC GAC AAA

D L Y Q L L S D R I H V L H P E G Y
GAC CTT TAC CAG CTC CTT TCC GAC CGC ATC CAC GTC CTC CAC CCC GAG GGG TAC

L I T P A W L W E K Y G L R P D Q W
CTC ATC ACC CCG GCC TGG CTT TGG GAA AAG TAC GGC CTG AGG CCC GAC CAG TGG

Replacement

Figure

A	N	L	W	G	R	L	E	G	E	R	L	L	W	L	Y	R
GCC	AAC	CTG	TGG	GGG	AGG	CTT	GAG	GGG	GAG	GAG	AGG	CTC	CTT	TGG	CTT	TAC
E	V	E	R	P	L	S	A	V	L	A	H	M	E	A	T	G
GAG	GTG	GAG	AGG	CCC	CTT	TCC	GCT	GCT	CTG	GCC	CAC	ATG	GAG	GCC	ACG	GGG
R	L	D	V	A	Y	L	R	A	L	S	L	E	V	A	E	I
CGC	CTG	GAC	GTG	GCC	TAT	CTC	AGG	GCC	TTG	TCC	CTG	GAG	GTG	GCC	GAG	ATC
A	R	L	E	A	E	V	F	R	L	A	G	H	P	F	N	N
GCC	CGC	CTC	GAG	GCC	GAG	GTC	TTC	CGC	CTG	GCC	GAC	CCC	TTC	AAC	CTC	AAC
S	R	D	Q	L	E	R	V	L	F	D	E	L	G	L	P	A
TCC	CGG	GAC	CAG	CTG	GAA	AGG	GTC	CTC	TTT	GAC	GAG	CTA	GGG	CTT	CCC	GCC
G	K	T	E	K	T	G	K	R	S	T	S	A	A	V	L	E
GGC	AAG	ACG	GAG	AAG	ACC	GGC	AAG	CGC	TCC	ACC	AGC	GCC	GCC	GTC	CTG	GAG
L	R	E	A	H	P	I	V	E	K	I	L	Q	Y	R	E	L
CTC	CGC	GAG	GCC	CAC	CCC	ATC	GTG	GAG	AAG	ATC	CTG	CAG	TAC	CGG	GAG	CTC
K	L	K	S	T	Y	I	D	P	L	P	D	L	I	H	P	R
AAG	CTG	AAG	AGC	ACC	TAC	ATT	GAC	CCC	TTG	CCG	GAC	CTC	ATC	CAC	CCC	AGG
G	R	L	H	T	R	F	N	Q	T	A	T	A	T	G	R	L
GGC	CGC	CTC	CAC	ACC	CGC	TTC	AAC	CAG	ACG	GCC	ACG	GCC	ACG	GGC	AGG	CTA
S	S	D	P	N	L	Q	N	I	P	V	R	T	P	L	G	Q
AGC	TCC	GAT	CCC	AAC	CTC	CAG	AAC	ATC	CCC	GTC	CGC	ACC	CCG	CTT	GGG	CAG
I	R	R	A	F	I	A	E	E	G	W	L	L	V	A	L	D
ATC	CGC	CGG	GCC	TTC	ATC	GCC	GAG	GAG	GGG	TGG	CTA	TTG	GTG	GCC	CTG	GAC
S	Q	I	E	L	R	V	L	A	H	L	S	G	D	E	N	L
AGC	CAG	ATA	GAG	CTC	AGG	GTG	CTG	GCC	CAC	CTC	TCC	GGC	GAC	GAG	AAC	CTG
R	V	F	Q	E	G	R	D	I	H	T	E	T	A	S	W	M

Replacement

Figure

CGG	GTC	TTC	CAG	GAG	GGG	CGG	GAC	ATC	CAC	ACG	GAG	ACC	GCC	AGC	TGG	ATG	TTC
G	V	P	R	E	A	V	D	P	L	M	R	R	A	A	K	T	I
GGC	GTC	CCC	CGG	GAG	GCC	GTG	GAC	CCC	CTG	ATG	CGC	CGG	GCG	GCC	AAG	ACC	ATC
N	F	G	V	L	Y	G	M	S	A	H	R	L	S	Q	E	L	A
AAC	TTC	GGG	GTC	CTC	TAC	GGC	ATG	TCG	GCC	CAC	CGC	CTC	TCC	CAG	GAG	CTA	GCC
I	P	Y	E	E	A	Q	A	F	I	E	R	Y	F	Q	S	F	P
ATC	CCT	TAC	GAG	GAG	GCC	CAG	GCC	TTC	ATT	GAG	CGC	TAC	TTT	CAG	AGC	TTC	CCC
K	V	R	A	W	I	E	K	T	L	E	E	G	R	R	R	G	Y
AAG	GTG	CGG	GCC	TGG	ATT	GAG	AAG	ACC	CTG	GAG	GAG	GGC	AGG	AGG	CGG	GGG	TAC
V	E	T	L	F	G	R	R	R	Y	V	P	D	L	E	A	R	V
GTG	GAG	ACC	CTC	TTC	GGC	CGC	CGC	TAC	GTG	CCA	GAC	CTA	GAG	GCC	CGG	GTG	
K	S	V	R	E	A	A	E	R	M	A	F	N	M	P	V	Q	G
AAG	AGC	GTG	CGG	GAG	GCG	GCC	GAG	CGC	ATG	GCC	TTC	AAC	ATG	CCC	GTC	CAG	GGC
T	A	A	D	L	M	K	L	A	M	V	K	L	F	P	R	L	E
ACC	GCC	GCC	GAC	CTC	ATG	AAG	CTG	GCT	ATG	GTG	AAG	CTC	TTC	CCC	AGG	CTG	GAG
E	M	G	A	R	M	L	L	Q	V	H	D	E	L	V	L	E	A
GAA	ATG	GGG	GCC	AGG	ATG	CTC	CTT	CAG	GTC	CAC	GAC	GAG	CTG	GTC	CTC	GAG	GCC
P	K	E	R	A	E	A	V	A	R	L	A	K	E	V	M	E	G
CCA	AAA	GAG	AGG	GCG	GAG	GCC	GTG	GCC	CGG	CTG	GCC	AAG	GAG	GTC	ATG	GAG	GGG
V	Y	P	L	A	V	P	L	E	V	E	V	G	I	G	E	D	W
GTG	TAT	CCC	CTG	GCC	GTG	CCC	CTG	GAG	GTG	GAG	GTG	GGG	ATA	GGG	GAG	GAC	TGG
L	S	A	K	E	G	I	D	G	R	G	G	G	H	H	H	H	H
CTC	TCC	GCC	AAG	GAG	GGC	ATT	GAT	GGC	CGC	GGA	GGC	GGG	CAT	CAT	CAT	CAT	CAT
H	H	//															
CAT	CAT	//															

Replacement

Figure

M	P	F	E	I	V	F	E	G	A	K	E	F	A	Q	L	I	D	18
ATG	CCA	TTT	GAA	ATC	GTA	TTT	GAA	GGT	GCA	AAA	GAG	TTT	GCC	CAA	CTT	ATA	GAC	54
T	A	S	K	L	I	D	E	A	A	F	K	V	T	E	D	G	I	36
ACC	GCA	AGT	AAG	TTA	ATA	GAT	GAG	GCC	GCG	TTT	AAA	GTT	ACA	GAA	GAT	GGG	ATA	108
S	M	R	A	M	D	P	S	R	V	V	L	I	D	L	N	L	P	54
AGC	ATG	AGG	GCC	ATG	GAT	CCA	AGT	AGA	GTT	GTC	CTG	ATT	GAC	CTA	AAT	CTC	CCG	162
S	S	I	F	S	K	Y	E	V	V	E	P	E	T	I	G	V	N	72
TCA	AGC	ATA	TTT	AGC	AAA	TAT	GAA	GTT	GTT	GAA	CCA	GAA	ACA	ATT	GGA	GTT	AAC	216
M	D	H	L	K	K	I	L	K	R	G	K	A	K	D	T	L	I	90
ATG	GAC	CAC	CTA	AAG	AAG	ATC	CTA	AAG	AGA	GGT	AAA	GCA	AAG	GAC	ACC	TTA	ATA	270
L	K	K	G	E	E	N	F	L	E	I	T	I	Q	G	T	A	T	108
CTC	AAG	AAA	GGA	GAG	GAA	AAC	TTC	TTA	GAG	ATA	ACA	ATT	CAA	GGA	ACT	GCA	ACA	324
R	T	F	R	V	P	L	I	D	V	E	E	M	E	V	D	L	P	126
AGA	ACA	TTT	AGA	GTT	CCC	CTA	ATA	GAT	GTA	GAA	GAG	ATG	GAA	GTT	GAC	CTC	CCA	378
E	L	P	F	T	A	K	V	V	V	L	G	E	V	L	K	D	A	144
GAA	CTT	CCA	TTC	ACT	GCA	AAG	GTT	GTA	GTT	CTT	GGA	GAA	GTC	CTA	AAA	GAT	GCT	432
V	K	D	A	S	L	V	S	D	S	I	K	F	I	A	R	E	N	162
GTT	AAA	GAT	GCC	TCT	CTA	GTG	AGT	GAC	AGC	ATA	AAA	TTT	ATT	GCC	AGG	GAA	AAT	486
E	F	I	M	K	A	E	G	E	T	Q	E	V	E	I	K	L	T	180
GAA	TTT	ATA	ATG	AAG	GCA	GAG	GGA	GAA	ACC	CAG	GAA	GTT	GAG	ATA	AAG	CTA	ACT	540
L	E	D	E	G	L	L	D	I	E	V	Q	E	E	T	K	S	A	198
CTT	GAA	GAT	GAG	GGA	TTA	TTG	GAC	ATC	GAG	GTT	CAA	GAG	GAG	ACA	AAG	AGC	GCA	594
Y	G	V	S	Y	L	S	D	M	V	K	G	L	G	K	A	D	E	216
TAT	GGA	GTC	AGC	TAT	CTC	TCC	GAC	ATG	GTT	AAA	GGA	CTT	GGA	AAG	GCC	GAT	GAA	648

Replacement

Figure

V	T	I	K	F	G	N	E	M	P	M	Q	M	E	Y	Y	I	R	234
GTT	ACA	ATA	AAG	TTT	GGA	AAT	GAA	ATG	CCC	ATG	CAA	ATG	GAG	TAT	TAC	ATT	AGA	702
D	E	G	R	L	T	F	L	L	A	P	R	V	E	E	*			250
GAT	GAA	GGA	AGA	CTT	ACA	TTC	CTA	CTG	GCT	CCA	AGA	GTT	GAA	GAG	TGA			

Figure 17W

Pfu DNA Polymerase (WT) -(PCNA) fusion protein

Nucleotide sequence (SEQ ID NO: 61) // Nucleotide sequence (SEQ ID NO: 67)

```

ccctggtcct gggtcacat atatgttctt actgccttt atgaagaatc cccagtcgc
tctaacctgg gttatagtga caaatcttcc tccaccaccg cccaagaagg ttatttctat
caactctaca cctcccctat tttctctctt atgagatttt taagtatagt tatagagaag
gttttatact ccaaaactgag ttagtagata tgtggggagc ataatgattt tagatgtgga
ttacataact gaagaaggaa aacctgttat taggctattc aaaaaagaga acggaaaatt
taagatagag catgatagaa ctttttagacc atacatttac gctcttctca gggatgattc
aaagattgaa gaagttaaga aaataacggg ggaaaggcat ggaaagattg tgagaattgt
tgatgtagag aagggtgaga aaaagtctt cggcaagcct attaccgtgt ggaaacttta
tttggaacat cccaagatg ttcccactat tagagaaaaa gttagagaac atccagcagt
tgtggacatc ttcgaatag atattccatt tgcaagaga tacctcatcg acaaaggcct

```

Replacement

Figure

aataccaatg gagggggaag aagagctaaa gattcttgcc. ttcgatatag aaaccctcta
tcacgaaggga gaagagttag gaaaaggccc aattataatg attagttatg cagatgaaaa
tgaaagcaaaag gtgattactt ggaaaaacat agatcttcca tacgttgagg ttgtatcaag
cgagagagag atgataaaga gatttctcag gattatcagg gagaaggatc ctgacattat
agttacttat aatggagact cattcgactt cccatattta gcgaaaaaggg cagaaaaact
tgggattaaa ttaaccattg gaagagatgg aagcgagccc aagatgcaga gaataggcga
tatgacggct gtagaagtca agggaagaat acatttcgac ttgtatcatg taataacaag
gacaataaat ctcccaacat acacactaga ggctgtatat gaagcaattt ttggaaagcc
aaaggagaag gtatacgccg acgagatagc aaaagcctgg gaaagtggag agaaccctga
gagagttgcc aaataactga tggaagatgc aaaggcaact tatgaactcg ggaaagaatt
ccttccaatg gaaattcagc tttcaagatt agttggaca cctttatggg atgtttcaag
gtcaagcaca gggaacccttg tagagtggtt cttacttagg aaagcctacg aaagaaacga
agtagctcca aacaagccaa gtgaagagga gtatcaaaga aggctcaggg agagctacac
agggtgattc gttaaagagc cagaaaaaggg gttgtgggaa aacatagtat acctagattt
tagagcccta tatccctcga ttataattac ccacaatgtt tctcccgata ctctaaatct
tgagggatgc aagaactatg atatcgctcc tcaagtaggc cacaagtctt gcaaggacat
ccctgggttt ataccaagtc tcttgggaca tttgttagag gaaagacaaa agattaagac
aaaaatgaag gaaactcaag atcctataga aaaaatactc cttgactata gacaaaaagc
gataaaactc ttagcaaatt ctttctacgg atattatggc tatgcaaaag caagatggta

Replacement

Figure

ctgtaaggag tgtgctgaga gcgttactgc ctggggaaga aagtacatcg agttagtatg
gaaggagctc gaagaaaaagt ttggatttaa agtcctctac attgacactg atggctctcta
tgcaactatc ccaggaggag aaagtgagga aataaaagaaa aaggctctag aatttgtaaa
atacataaat tcaaagctcc ctggactgct agagcttgaa tatgaagggt ttataagag
gggattcttc gttacgaaga agaggtatgc agtaatagat gaagaaggaa aagtcattac
tcgtggttta gagatagtta ggagagattg gagtgaatt gcaaaagaaa ctcaagctag
agttttggag acaatactaa aacacggaga tgttgaagaa gctgtgagaa tagtaaaaga
agtaatacaa aagcttgcca attatgaaat tccaccagag aagctcgcaa tatatgagca
gataacaaga ccattacatg agtataaggc gataggtcct cacgtagctg ttgcaaaagaa
actagctgct aaaggagtta aaataaagcc aggaatggta attggataca tagtacttag
aggcgatggt ccaattagca atagggcaat tctagctgag gaatacgatc ccaaaaagca
caagtatgac gcagaatat acattgagaa ccaggttctt ccagcggtag ttaggatatt
ggagggattt ggatacagaa aggaagacct cagataccaa aagacaagac aagtcggcct
aacttcctgg cttaacatta aaaaatccta gaaaagcgat agatatcaac ttttatcttt
tctaaacctt ttctatgaa gaagaactga gcaggaatta ccagttcttc cgttatttta
tgggtaatta aaaaccatg ctcttgggag aatcttcgaa taaaatccct aacttcaggc
tttgctaagt gaatagaata aacaacatca ctcacttcaa acgccttcgt tagaaatggt
ctatctgcat gcttctctgg ctcggaanng gaggattcat aacaacagta tcaacattct
cagagaattg agaaacatca gaaactttga ctctacaac atttctaact ttgcaactct

Replacement

Figure

tcaagatttt	ctaaaagaat	tttaacgggc	tcctcgtcaa	tttcgacgac	gtagatcttt	
tttgctccaa	gcagagccgc	tccaatggat	aacaccctg	ttcccgacc	caagtcgct	
acaatttttt	ccttgatatct	cctaattgtat	aagcaagcca	aaggagagta	gatgctacct	
ttccgggagt	tttgatttgc	tctagccaag	gtttgggatt	tttgaatcct	ttactctgg	
aaagtataat	ttcaagctcc	ttcttcttca	tgacagatga	aaaattgttt	tgtctctttt	
taacttttac	agaaaataact	gtctcaaatt	atgacaaactc	ttgacatttt	tacttcatta	
ccagggtaat	gtttttaagt	atgaaaatttt	tctttcatag	aggaggnnnn	nngtcctctc	
ctcgatttcc	ttggttgtgc	tccatatgat	aagcttccaa	agtgggtgtt	cagactttta	
gacactcaaa	taccagacga	caatgggtgtg	ctcactcaag	ccccatatgg	gttgagaaaa	
gtagaagcgg	cactactcag	atgcttcccc	aggaatgagg	ttgttgtagc	tcntcccnga	
aagattgaga	tgttcttgg	//				
ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC						54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA						108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG						162
TCA AGC ATA TTT AGC AAA TAT GAA GTT GTT GAA CCA GAA ACA ATT GGA GTT AAC						216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA						270
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA						324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA						378
GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT						432
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT						486
GAA TTT ATA ATG AAG GCA GAG GGA GAA ACC CAG GAA GTT GAG ATA AAG CTA ACT						540
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA						594
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA						648
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA						702
GAT GAA GGA AGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG TGA						

Replacement

Figure

Figure 17X

(PCNA) - Pfu DNA Polymerase (WT) fusion protein

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 61)

ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC	54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA	108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG	162
TCA AGC ATA TTT AGC AAA TAT GAA GAT GTT GAA CCA GAA ACA ATT GGA GTT AAC	216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA	270
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA	324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA	378
GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT	432
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT	486
GAA TTT ATA ATG AAG GCA GAG GGA GAA ACC CAG GAA GTT GAG ATA AAG CTA ACT	540
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA	594
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA	648
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA	702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG	

ccctggtcct gggtcacat atatgttctt actgccttt atgaagaatc cccagtcgc
tctaacctgg gttatagtga caaatcttcc tcaccaccg cccaagaagg ttatttctat
caactctaca cctccccat tttctctctt atgagatttt taagtatagt tatagagaag
gttttatact ccaaaactgag ttagtagata tgtggggagc ataatgattt tagatgtgga
ttacataact gaagaaggaa aacctgttat taggtattc aaaaaagaga acggaaaatt

Replacement

Figure

taagatagag catgatagaa ctttttagacc atacatttac gctcttctca gggatgattc
aaagattgaa gaagttaaga aaataacggg ggaaaggcat ggaaagattg tgagaattgt
tgatgtagag aaggttgaga aaaagtctct cggaagcct attaccgtgt ggaaaactta
tttggaacat cccaagatg ttccactat tagagaaaa gtagagAAC atccagcagt
tgtggacatc ttcgaatacg atattccatt tgcaagaga tacctcatcg acaaggcct
aataccaatg gagggggaag aagagctaaa gattcttgcc ttcgatatag aaaccctcta
tcacgaagga gaagagtctg gaaaaggccc aattataatg attagttatg cagatgaaaa
tgaaagcaag gtgattactt ggaaaaacat agatcttcca tacgttgagg ttgtatcaag
cgagagagag atgataaaga gatttctcag gattatcagg gagaaggatc ctgacattat
agttacttat aatggagact cattcgactt cccatatcta gcgaaaaagg cagaaaaact
tgggattaaa ttaaccattg gaagagatgg aagcgagccc aagatgcaga gaataggcga
tatgacggct gtagaagtca agggaagaat acatttcgac ttgtatcatg taataacaag
gacaataaat ctccaacat acacactaga ggctgtatat gaagcaattt ttggaaagcc
aaaggagaag gtatacgccg acgagatagc aaagcctgg gaaagtggag agaaccctga
gagagttgcc aaatactcga tggaagatgc aaaggcaact tatgaactcg ggaaagaatt
ccttccaatg gaaattcagc tttcaagatt agttggaca ctttatggg atgtttcaag
gtcaagcaca gggaaccttg tagagtggtt ctacttagg aaagcctacg aaagaaacga
agtagctcca aacaagccaa gtgaagagga gtatcaaga aggtcaggg agagctacac
aggtggattc gttaaagac cagaaaaagg gtgtgggaa aacatagtat acctagattt

Replacement

Figure

tagagcccta tatccctcga ttataattac ccacaatggt tctcccgata ctctaaatct
tgagggatgc aagaactatg atatcgctcc tcaagtaggc cacaagttct gcaaggacat
ccctgggttt ataccaagtc tcttgggaca ttgttagag gaaagacaaa agattaagac
aaaaatgaag gaaactcaag atcctataga aaaatactc ctgactata gacaaaaagc
gataaaactc ttagcaaat ctttctacgg atattatggc tatgcaaaag caagatggta
ctgtaaggag tgtgctgaga gcgttactgc ctggggaaga aagtacatcg agttagtatg
gaaggagctc gaagaaaagt ttggatttaa agtcctctac attgacactg atggtctcta
tgcaactatc ccaggaggag aaagtgagga aataaagaaa aaggctctag aatttgtaaa
atacataaat tcaaagctcc ctggactgct agagcttgaa tatgaagggt ttataagag
gggattcttc gttacgaaga agaggtatgc agtaatagat gaagaaggaa aagtcattac
tcgtgggtta gagatagtta ggagagattg gagtgaatt gcaaaagaaa ctcaagctag
agttttggag acaatactaa aacacggaga tgttgaagaa gctgtgagaa tagtaaaaga
agtaatacaa aagcttgcca attatgaaat tccaccagag aagctcgcaa tatatgagca
gataacaaga ccattacatg agtataaaggc gataggctct cacgtagctg ttgcaaaagaa
actagctgct aaaggagtta aaataaagcc aggaatggta attggataca tagtacttag
aggcgatggt ccaattagca atagggcaat tctagctgag gaatacgatc ccaaaaagca
caagtatgac gcagaatatt acattgagaa ccaggttctt ccagcggtag ttaggatatt
ggagggattt ggatacagaa aggaagacct cagataccaa aagacaagac aagtcggcct
aacttcctgg cttaacatta aaaatccta gaaaagcgat agatatcaac ttttattctt

Replacement

Figure

tctaaccctt ttctatgaaa gaagaactga gcaggaatta ccagttcttc cgttatttta
tgggtaatta aaaacccatg ctcttgggag aatcttcgaa taaaatccct aacttcaggc
tttgctaagt gaatagaata aacaacatca ctcaactcaa acgccttcgt tagaaaatggt
ctatctgcat gcttctcttg ctcggaanng gaggattcat aacaacagta tcaacattct
cagagaattg agaaacatca gaaactttga ctctacaac atttctaact ttgcaactct
tcaagatttt ctaaaagaat tttaacggcc tcctcgtcaa tttcgacgac gtagatcttt
tttgctcaa gcagagccgc tccaatggat aacaccctg tccccgacc caagtccgct
acaattttt ccttgatatc cctaattgat aagcaagcca aaggagagta gatgctacct
ttccgggagt tttgtattgc tctagccaag gtttgggatt tttegaacct ttaactctgg
aaagtataat ttcaagctcc ttcttcttca tgacagatga aaaattgttt tgtctctttt
taacttttac agaaataact gtctcaaatt atgacaactc ttgacatttt tacttcatta
ccagggtaat gtttttaagt atgaaatttt tctttcatag aggaggnnnn nngtcctctc
ctcgatttcc ttgggttgtc tccatatgat aagcttccaa agtgggtgtt cagactttta
gacactcaaa taccagacga caatggtgtg ctcaactcaag cccatatgg gttgagaaaa
gtagaagcgg cactactcag atgcttcccc aggaatgagg ttgttgtagc tcntcccnga
aagattgaga tgttcttgg // TGA

Figure 17Y

Replacement

Figure

(PCNA) - PFU DNA POLYMERASE (V93 R OR E) fusion protein

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 27)
Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 28)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC	54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA	108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG	162
TCA AGC ATA TTT AGC AAA TAT GAA GTT GAA CCA GAA ACA ATT GGA GTT AAC	216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA	270
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA	324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA	378
GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT	432
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT	486
GAA TTT ATA ATG AAG GCA GAG GGA ACC CAG GAA GTT GAG ATA AAG CTA ACT	540
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA	594
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA	648
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA	702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG //	

ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATXXXC CCACTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTGTC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAAGAT TCTTGCC TTC 420
GATATAGAAA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAATGA AGCAAAAGGTG ATTA CTGGA AAAACATAGA TCTTCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600

Replacement

Figure


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AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCTC ATATTAGCG 660
AAAAGGGCAG AAAAAGCTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTTG GAAAGCCAAA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 1020
GAACTCGGGA AAGAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1080
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1140
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGAGTA TCAAGAAGAG 1200
CTCAGGGAGA GCTACACAGG TGGATTTCGT AAAGAGCCAG AAAAGGGGT GTGGGAAAAC 1260
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1320
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1380
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1440
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAA AATACTCCTT 1500
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCCT TCTACGGATA TTATGGCTAT 1560
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTAAGTCCCTG GGAAGAAAAG 1620
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACAT 1680
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAG 1740
GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1800
GAAGGGTTTT ATAAGAGGGG ATTCTTTCGTT ACGAAGAAAG GGTATGCAGT AATAGATGAA 1860
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAATTTGCA 1920
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1980
GTGAGAATAG TAAAGAAGT AATACAAAAG CTGCCCAAT ATGAAATTCC ACCAGAGAAG 2040
CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGTCCCTCAC 2100
GTAGCTGTTG CAAAGAACT AGCTGCTAAA GGAGTTAAA GAGTCCAGG AATGGTAAT 2160
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGCATTTCT AGCTGAGGAA 2220
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTCTTCCA 2280
GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAAG AAGACCTCAG ATACCAAAG 2328
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAATA AATCC //
// TGA

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Figure 17Z

PFU DNA POLYMERASE (V93 R OR E) -(PCNA) fusion protein

Replacement

Figure

Nucleotide sequence (SEQ ID NO: 27) // Nucleotide sequence (SEQ ID NO: 67)
Nucleotide sequence (SEQ ID NO: 28) // Nucleotide sequence (SEQ ID NO: 67)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60
AAAGAGAAACG GAAAATTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTACGCT 120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAA TAACGGGGA AAGCATGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAAG GTTGAGAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATT GGAACATCCC CAAGATXXX CCACTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCCTC 420
GATATAGAAA CCTCTATCA CGAAGGAGAA GAGTTTGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAATGA AGCAAAAGTG ATTACTTGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCC ATATTAGCG 660
AAAAGGGCAG AAAAAGTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTGG GAAAGCCAAA GGAGAAAGTA TACGCCGACG AGATAGCAA AGCCTGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAA GGCAACTTAT 960
GAACTCGGGA AAGAATTCCT TCCAATGGAA ATTCAAGTTT CAAGATTAGT TGGACACCTT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGAGTA TCAAGAAGG 1140
CTCAGGGAGA GCTACACAGG TGGATTTCGT AAAGAGCCAG AAAAGGGTT GTGGGAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAACTCTTA GCAAATTCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTAAGTCCCTG GGAAGAAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAG 1680
GCTCTAGAA TTTGTAATAA CATAAATTCA AAGTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800

Replacement

Figure

GAAGGAAAAG	TCATTACTCG	TGGTTTAGAG	ATAGTTAGGA	GAGATTGGAG	TGAAATTGCA	1860
AAAGAAACTC	AAGCTAGAGT	TTTGGAGACA	ATACTAAAAC	ACGGAGATGT	TGAAGAAGCT	1920
GTGAGAATAG	TAAAAGAAGT	AATACAAAAG	CTTGCCCAATT	ATGAAATTCC	ACCAGAGAAG	1980
CTCGCAATAT	ATGAGCAGAT	AACAAGACCA	TTACATGAGT	ATAAGGCGAT	AGGTCCCTCAC	2040
GTAGCTGTTG	CAAAGAAACT	AGCTGCTAAA	GGAGTTAAAA	TAAAGCCAGG	AATGGTAATT	2100
GGATACATAG	TACTTAGAGG	CGATGGTCCA	ATTAGCAATA	GGCAATTCT	AGCTGAGGAA	2160
TACGATCCCA	AAAAGCACAA	GTATGACGCA	GAATATTACA	TGGAGAACCA	GGTTCTTTCCA	2220
GCGGTACTTA	GGATATTGGA	GGGATTTGGA	TACAGAAAAG	AAGACCTCAG	ATACCAAAAG	2280
ACAAGACAAG	TCGGCCTAAC	TTCTGGGCTT	AACATTAAAA	AATCC //		2328

ATG CCA	TTT GAA	ATC GTA	TTT GAA	GGT GCA	AAA GAG	TTT GCC	CAA CTT	ATA GAC	54
ACC GCA	AGT AAG	TTA ATA	GAT GAG	GCC GCG	TTT AAA	GTT ACA	GAA GAT	GGG ATA	108
AGC ATG	AGG GCC	ATG GAT	CCA AGT	AGA GTT	GTC CTG	ATT GAC	CTA AAT	CTC CCG	162
TCA AGC	ATA TTT	AGC AAA	TAT GAA	GTT GAT	GAA CCA	GAA ACA	ATT GGA	GTT AAC	216
ATG GAC	CAC CTA	AAG AAG	ATC CTA	AAG AGA	GGT AAA	GCA AAG	GAC ACC	TTA ATA	270
CTC AAG	AAA GGA	GAG GAA	AAC AAC	TTC TTA	GAG ATA	ACA ATT	CAA GGA	ACT GCA	324
AGA ACA	TTT AGA	GTT CCC	CTA ATA	GAT GTA	GAA GAG	ATG GAA	GTT GAC	CTC CCA	378
GAA CTT	CCA TTC	ACT ACT	GCA AAG	GTT GTA	GTT CTT	GGA GAA	GTC CTA	AAA GAT	432
GTT AAA	GAT GCC	TCT CTA	GTG AGT	GAC AGC	ATA AAA	TTT ATT	GCC AGG	GAA AAT	486
GAA TTT	ATA ATG	AAG GCA	GAG GGA	GAA ACC	CAG GAA	GTT GAG	ATA AAG	CTA ACT	540
CTT GAA	GAT GAG	GGA TTA	TTG GAC	ATC GAG	GTT CAA	GAG GAG	ACA AAG	AGC GCA	594
TAT GGA	GTC AGC	TAT CTC	TCC GAC	ATG GAT	GTT AAA	GGA CTT	GGA AAG	GCC GAT	648
GTT ACA	ATA AAG	TTT GGA	AAT GAA	ATG CCC	ATG CAA	ATG GAG	TAT TAC	ATT AGA	702
GAT GAA	GGA AGA	CTT ACA	TTC CTA	CTG GCT	CCA AGA	GTT GAA	GAG TGA		

Figure 17AA

PFU DNA POLYMERASE (G387P/V93R OR E) -(PCNA) fusion protein

Nucleotide sequence (SEQ ID NO: 29) // Nucleotide sequence (SEQ ID NO: 67)
Nucleotide sequence (SEQ ID NO: 30) // Nucleotide sequence (SEQ ID NO: 67)

Replacement

Figure

G387P Mutant (CCN is the codon for Proline where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTAGAGAAAG AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATXXXC CCACTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCCTC 420
GATATAGAAA CCTCTCTATCA CGAAGGAGAA GAGTTTGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAAATGA AGCAAAGGTG ATTACTTGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCC ATATTTAGCG 660
AAAAGGGCAG AAAA~~ACT~~TGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGCGGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTGT GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
GAACTCGGGA AAGAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAAG 1140
CTCAGGGAGA GCTACACACC NGGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA AAAAATTTCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTA~~CT~~GCCTG GGAAGAAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAA~~AA~~AG 1680
GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGA~~AA~~TTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980

Replacement

Figure

CTCGCAATAT ATGAGCAGAT AACAAAGACCA TTACATGAGT ATAAGGCGAT AGTCTCTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GTTCTTTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC // 2328

ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC	54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GAT GAA GAT GGG ATA	108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG	162
TCA AGC ATA TTT AGC AAA TAT GAA GTT GTT GAA CCA GAA ACA ATT GGA GTT AAC	216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA	270
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA	324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA	378
GAA CTT CCA TTC ACT TCT CTA AAG GCA AAG GTT GTA GTT GGA GAA GTC CTA AAA GAT GCT	432
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT	486
GAA TTT ATA ATG AAG GCA GAG GGA ACC CAG GAA GTT GAG ATA AAG CTA ACT	540
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GAG GAG ACA AAG AGC GCA	594
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA	648
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA	702
GAT GAA GGA AGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG TGA	

Figure 17BB

(PCNA) - PFU DNA POLYMERASE (G387P/V93R OR E) fusion protein

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 29)

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 30)

G387P Mutant (CCN is the codon for Proline where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

Replacement

Figure

ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC 54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA 108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG 162
TCA AGC ATA TTT AGC AAA TAT GAA GTT GAA CCA GAA ACA ATT GGA GTT AAC 216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA 270
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA 324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA 378
GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT 432
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT 486
GAA TTT ATA ATG AAG GCA GAG GGA GAA ACC CAG GAA GTT GAG ATA AAG CTA ACT 540
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA 594
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA 648
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA 702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG //

ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTACGCT 120
CTTCTCAGGG ATGATTCAA GATTGAAGAA GTTAAGAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTGTA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATXXXC CCACATATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCCTC 420
GATATAGAAA CCCTCTATCA CGAAGGAGAA GAGTTTGGA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAAATGA AGCAAAGGTG ATTACTTGG AACAATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTTCC ATATTTAGCG 660
AAAAGGGCAG AAAAACTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTGG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGA 900
AGTGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
GAACTCGGGA AAGAAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAGGTC AAGCACAGGG AACCTTGTA AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140
CTCAGGGAGA GCTACACACC NGGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320

Replacement

Figure

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AAGTCTTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAAATCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCCTG GGAAGAGAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAGTTTG GATTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTTCGT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAATTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCCTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTCTTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAAG AAGACCTCAG ATACCAAAAG 2280
ACAAAGACAAG TCGGCCCTAAC TTCCTGGCTT AACATTAAAA AATCC //TAG 2328

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Figure 17CC

(PCNA) - PFU DNA POLYMERASE(D141A/E143A/V93R OR E) fusion protein

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 31)

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 32)

D141A/E143A Mutant (GCN is the codon for alanine where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATG CCA	TTT GAA	ATC GTA	TTT GAA	GGT GCA	AAA GAG	TTT GCC	CAA CTT	ATA GAC	54
ACC GCA	AGT AAG	TTA ATA	GAT GAG	GCC GCG	TTT AAA	GTT ACA	GAA GAT	GGG ATA	108
AGC ATG	AGG GCC	ATG GAT	CCA AGT	AGA GTT	GTC CTG	ATT GAC	CTA AAT	CTC CCG	162
TCA AGC	ATA TTT	AGC AAA	TAT GAA	GTT GTT	GAA CCA	ACA ATT	GGA GTT	AAC	216

Replacement

Figure

ATG GAC CAC CTA AAG AAG AAG AAG AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA 270
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA 324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA 378
GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT 432
GTT AAA GAT GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT 486
GAA TTT ATA ATG AAG GCA GAG GGA GAA ACC CAG GAA GTT GAG ATA AAG CTA ACT 540
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG ACA AAG AGC GCA 594
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA 648
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA 702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG //

//ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAAC CTGTTATTAG GCTATTCAA 60
AAAGAGAACG GAAAAATTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTACGCT 120
CTTCTCAGGG ATGATTTCAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAA GGTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATXXXC CCACATATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCCTC 420
GCNATAGCNA CCTCTATCA CGAAGGAGAA GAGTTTGAA AAGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAAATGA AGCAAAGGTG ATTACTTTGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCC ATATTTAGCG 660
AAAAGGCAG AAAAAGCTGG GATTAAATTA ACCATTGGA AGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAAG GAAGAATACA TTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTGG GAAAGCCAAA GGAGAAAGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
GAACTCGGGA AAGAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAGGTC AAGCACAGGG AACCTTGTA AGTGGTTCTT ACTTAGGAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGT AAGAGGAGTA TCAAAGAAGG 1140
CTCAGGGAGA GCTACACA GTT_GGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCGCA AGGACATCCC TGGTTTATA CCAAGTCTCT TGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCCT TCTACGGATA TTATGGCTAT 1500
GCAAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCCTG GGAAGAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTAAAGT CCTCTACATT 1620

Replacement

Figure

GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGA AATTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAC ACGGAGATGT TGAAGAAAGCT 1920
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGC AATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTCTCTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAA AATCC // 2328
TGA

Figure 17DD

PFU DNA POLYMERASE(D141A/E143A/V93R OR E) - (PCNA) fusion protein

Nucleotide sequence (SEQ ID NO: 31) // Nucleotide sequence (SEQ ID NO: 67)

Nucleotide sequence (SEQ ID NO: 32) // Nucleotide sequence (SEQ ID NO: 67)

D141A/E143A Mutant (GCN is the codon for alanine where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAAC CTGTTATTAG GCTATTCAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTACGCT 120
CTTCTCAGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGA AAGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATXXXC CCACTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTGTC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420
GCNATAGCNA CCCTCTATCA CGAAGGAGAA GAGTTTGGA AAGGCCCAAT TATAATGATT 480

Replacement

Figure

AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TCTTCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTTCC ATATTTAGCG 660
AAAAGGCAG AAAAACTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
TATCATGTAA TAAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTGG GAAAGCCCAA GGAGAAAGTA TACGCCGACG AGATAGCAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAA GGCAACTTAT 960
GAACTCGGGA AGAATTTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGAGTA TCAAAGAAGG 1140
CTCAGGGAGA GCTACACA GTT_GGATTTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTATA CCAAGTCTCT TGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCCT TCTACGGATA TTATGGCTAT 1500
GCAAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCCTG GGAAGAAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAATATGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCCTCAC 2040
GTAGCTGTTG CAAAAGAACT AGCTGCTAAA GGAGTTAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTCTTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAAGG AAGACCTCAG ATACCAAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCTGGCTT AACATTAAA AATCC // 2328

ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC	54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA	108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG	162
TCA AGC ATA TTT AGC AAA TAT GAA GTT GAA CCA GAA ACA ATT GGA GTT AAC	216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA	270
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA	324

Replacement

Figure

AGA	ACA	TTT	AGA	GTT	CCC	CTA	ATA	GAT	GTA	GAA	GAG	ATG	GAA	GTT	GAC	CTC	CCA	378
GAA	CTT	CCA	TTC	ACT	GCA	AAG	GTT	GTA	GTT	CTT	GGA	GAA	GTC	CTA	AAA	GAT	GCT	432
GTT	AAA	GAT	GCC	TCT	CTA	GTG	AGT	GAC	AGC	ATA	AAA	TTT	ATT	GCC	AGG	GAA	AAT	486
GAA	TTT	ATA	ATG	AAG	GCA	GAG	GGA	GAA	ACC	CAG	GAA	GTT	GAG	ATA	AAG	CTA	ACT	540
CTT	GAA	GAT	GAG	GGA	TTA	TTG	GAC	ATC	GAG	GTT	CAA	GAG	GAG	ACA	AAG	AGC	GCA	594
TAT	GGA	GTC	AGC	TAT	CTC	TCC	GAC	ATG	GTT	AAA	GGA	CTT	GGA	AAG	GCC	GAT	GAA	648
GTT	ACA	ATA	AAG	TTT	GGA	AAT	GAA	ATG	CCC	ATG	CAA	ATG	GAG	TAT	TAC	ATT	AGA	702
GAT	GAA	GGA	AGA	CTT	ACA	TTC	CTA	CTG	GCT	CCA	AGA	GTT	GAA	GAG	TGA			

Figure 17EE

KOD DNA POLYMERASE - (PCNA) fusion protein

Nucleotide sequence (SEQ ID NO: 33) // Nucleotide sequence (SEQ ID NO: 67)
Nucleotide sequence (SEQ ID NO: 34) // Nucleotide sequence (SEQ ID NO: 67)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
ATGATCCTCG ACACTGACTA CATAACCGAG GATGGAAGC CTGTCATAAG AATTTC AAG 60
AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT TTGAAACCCTA CTTCTACGCC 120
CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAAGA TAACCGCCGA GAGGCACGGG 180
ACGGTTGTAA CGGTTAAGCG GGTGAAAAG GTTCAGAAGA AGTTCCTCGG GAGACCAGTT 240
GAGGTCTGGA AACTCTACTT TACTCATCCG CAGGACXXC CAGCGATAAG GGACAAGATA 300
CGAGAGCATC CAGCAGTTAT TGACATCTAC GAGTACGACA TACCCTTCGC CAAGCGCTAC 360
CTCATAGACA AGGGATTAGT GCCAATGGAA GCGACGAGG AGCTGAAAAT GCTCGCCTTC 420
GACATTGAAA CTCTCTACCA TGAGGGCGAG GAGTTCGCCG AGGGCCAAT CCTTATGATA 480
AGCTACGCCG ACGAGGAAGG GGCCAGGGTG ATAACTTGGG AGAACGTGGA TCTCCCCTAC 540
GTTGACGTCG TCTCGACGGA GAGGGAGATG ATAAAGCGCT TCCTCCGTGT TGTGAAGGAG 600
AAAGACCCCG ACGTTCTCAT AACCTACAAC GCGACAAC TCGACTTCGC CTATCTGAAA 660
AAGCGCTGTG AAAAGCTCGG AATAAACTTC GCCCTCGGAA GGGATGGAAG CGAGCCGAAG 720
ATTTCAGAGGA TGGGCGACAG GTTTGCCGTC GAAGTGAAGG GACGGATACA CTTCGATCTC 780
TATCCTGTGA TAAGACGGAC GATAAACCTG CCCACATACA CGCTTGAGGC CGTTTATGAA 840
GCCGTCTTCG GTCAGCCGAA GGAGAAGGTT TACGCTGAGG AAATAACCAC AGCCTGGGAA 900
ACCGGCGAGA ACCTTGAGAG AGTCGCCCGC TACTCGATGG AAGATGCGAA GGTCAACATAC 960

Replacement

Figure

GAGCTTGGGA	AGGAGTTCCT	TCCGATGGAG	GCCCAGCTTT	CTCGCTTAAT	CGGCCAGTCC	1020			
CTCTGGGACG	TCTCCCGCTC	CAGCACTGGC	AACCTCGTTG	AGTGGTTCCT	CCTCAGGAAG	1080			
GCCTATGAGA	GGAATGAGCT	GGCCCCGAAC	AAGCCCGATG	AAAAGGAGCT	GGCCAGAAGA	1140			
CGGCAGAGCT	ATGAAGGAGG	CTATGTAAAA	GAGCCCAGAG	GAGGGTTGTG	GGAGAACATA	1200			
GTGTACCTAG	ATTTTAGATC	CCTGTACCCC	TCAATCATCA	TCACCCACAA	CGTCTCGCCG	1260			
GATACGCTCA	ACAGAGAAGG	ATGCAAGGAA	TATGACGTTG	CCCCACAGGT	CGGCCACCGC	1320			
TTCTGCAAGG	ACTTCCCAGG	ATTTATCCCG	AGCCTGCTTG	GAGACCTCCT	AGAGGAGAGG	1380			
CAGAAGATAA	AGAAGAAGAT	GAAGGCCACG	ATTGACCCGA	TCGAGAGGAA	GCTCCTCGAT	1440			
TACAGGCAGA	GGGCCATCAA	GATCCTGGCA	AACAGCTACT	ACGGTTACTA	CGGCTATGCA	1500			
AGGGCGCGCT	GGTACTGCAA	GGAGTGTGCA	GAGAGCGTAA	CGGCCTGGGG	AAGGGAGTAC	1560			
ATAACGATGA	CCATCAAGGA	GATAGAGGAA	AAGTACGGCT	TTAAGGTAAT	CTACAGCGAC	1620			
ACCGACGGAT	TTTTTGCCAC	AATACCTGGA	GCCGATGCTG	AAACCGTCAA	AAAGAAAGGCT	1680			
ATGGAGTTCC	TCAAGTATAT	CAACGCCAAA	CTTCCGGGCG	CGCTTGAGCT	CGAGTACGAG	1740			
GGCTTCTACA	AACGCGGCTT	CTTCGTACAG	AAGAAGAAGT	ATGCGGTGAT	AGACGAGGAA	1800			
GGCAAGATAA	CAACGCGCGG	ACTTGAGATT	GTGAGGCGTG	ACTGGAGCGA	GATAGCGAAA	1860			
GAGACGCAGG	CGAGGGTTCT	TGAAGCTTTG	CTAAAGGACG	GTGACGTCGA	GAAGGCCGTG	1920			
AGGATAGTCA	AAGAAGTTAC	CGAAAAGCTG	AGCAAGTACG	AGGTTCCGCC	GGAGAAAGCTG	1980			
GTGATCCACG	AGCAGATAAC	GAGGGATTTA	AAGGACTACA	AGGCAACCGG	TCCCCACGTT	2040			
GCCGTTGCCA	AGAGGTTGGC	CGCGAGAGGA	GTCAAAATAC	GCCCTGGAAC	GGTGATAAGC	2100			
TACATCGTGC	TCAAGGGCTC	TGGGAGGATA	GGCGACAGGG	CGATACCGTT	CGACGAGTTC	2160			
GACCCGACGA	AGCACAAAGTA	CGACGCCGAG	TACTACATTG	AGAACCAGGT	TCTCCCAGCC	2220			
GTTGAGAGAA	TTCTGAGAGC	CTTCGGTTAC	CGCAAGGAA	ACCTGCGCTA	CCAGAAGACG	2280			
AGACAGGTTG	GTTTGAGTGC	TTGGCTGAAG	CCGAAGGGAA	CT	2325				
ATG CCA	TTT GAA	ATC GTA	TTT GAA	GGT GCA	AAA GAG	TTT GCC	CAA CTT	ATA GAC	54
ACC GCA	AGT AAG	TTA ATA	GAT GAG	GCC GCG	TTT AAA	GTT ACA	GAA GAT	GGG ATA	108
AGC ATG	AGG GCC	ATG GAT	CCA AGT	AGA GGT	GTC GCG	ATT GAC	CTA AAT	CTC CCG	162
TCA AGC	ATA TTT	AGC AAA	TAT GAA	GTT GAA	CCA GAA	ACA ATT	GGA GAT	GTT AAC	216
ATG GAC	CAC CTA	AAG AAG	ATC CTA	AAG AGA	GGT AAA	GCA AAG	GAC ACC	TTA ATA	270
CTC AAG	AAA GGA	GAG GAA	AAC TTC	TTA GAG	ATA ACA	ATT CAA	GGA ACT	GCA ACA	324
AGA ACA	TTT AGA	GTT CCC	CTA ATA	GAT GTA	GAA GAG	ATG GAA	GTT GAC	CTC CCA	378
GAA CTT	CCA TTC	ACT GCA	AAG GGT	GTA GGT	CTT GAA	GAA GTC	CTA AAA	GAT GCT	432
GTT AAA	GAT GCC	TCT CTA	GTG AGT	GAC AGC	ATA AAA	TTT ATT	GCC AGG	GAA AAT	486
GAA TTT	ATA ATG	AAG AAG	GCA GAG	GGA ACC	CAG GAA	GTT GAG	ATA AAG	CTA ACT	540
CTT GAA	GAT GAG	GGA TTA	TTG GAC	ATC GAG	GTT CAA	GAG GAG	ACA AAG	AGC GCA	594
TAT GGA	GTC AGC	TAT CTC	TCC GAC	ATG GAT	GTT AAA	GGA CTT	GGA AAG	GCC GAT	648
GTT ACA	ATA AAG	TTT GGA	AAT GAA	ATG CCC	ATG CAA	ATG GAG	TAT TAC	ATT AGA	702
GAT GAA	GGA AGA	CTT ACA	TTC CTA	CTG GCT	CCA AGA	GTT GAA	GAG TGA		

Replacement

Figure

Figure 17FF

(PCNA) - KOD DNA POLYMERASE fusion protein

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 33)

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 34)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC	54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA	108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG	162
TCA AGC ATA TTT AGC AAA TAT GAA GTT GAA CCA GAA ACA ATT GGA GTT AAC	216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA	270
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA	324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA	378
GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT GGA GAA GTC CTA AAA GAT GCT	432
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT	486
GAA TTT ATA ATG AAG GCA GAG GGA ACC CAG GAA GTT GAG ATA AAG CTA ACT	540
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA	594
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA	648
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA	702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG //	

ATGATCCTCG	ACACTGACTA	CATAACCGAG	GATGGAAGC	CTGTCATAAG	AATTTCAAG	60
AAGGAAAACG	GCGAGTTTAA	GATTGAGTAC	GACCGGACTT	TTGAACCCCTA	CTTCTACGCC	120
CTCCTGAAGG	ACGATTCTGC	CATTGAGGAA	GTCAAGAAGA	TAACCGCCGA	GAGGCACGGG	180
ACGGTTGTAA	CGGTTAAGCG	GGTTGAAAAG	GTTCAGAAGA	AGTTCCTCGG	GAGACCAGTT	240
GAGGCTGGA	AACTCTACTT	TACTCATCCG	CAGGACXXC	CAGCGATAAG	GGACAAAGATA	300
CGAGAGCATC	CAGCAGTTAT	TGACATCTAC	GAGTACGACA	TACCCCTTCG	CAAGCGCTAC	360
CTCATAGACA	AGGGATTAGT	GCCAATGGAA	GGCGACGAGG	AGCTGAAAAT	GCTCGCCTTC	420

Replacement

Figure

GACATTGAAA CTCTCTACCA TGAGGGCGAG GAGTTCGCCG AGGGCCCAAT CCTTATGATA 480
AGCTACGCCG ACGAGGAAGG GGCCAGGGTG ATAACTTGA AGAACGTGA TCTCCCCTAC 540
GTTGACGTG TCTCGACGGA GAGGAGATG ATAAAGCGCT TCTCCGTGT TGTAAAGGAG 600
AAAGACCCGG ACGTTCTCAT AACCTACAAC GCGACAAC TCGACTTCGC CTATCTGAAA 660
AAGCGCTGTG AAAAGCTCGG AATAAACTTC GCCCTCGAA GGGATGGAAG CGAGCCGAAG 720
ATTGAGAGGA TGGGCGACAG GTTTGCCGTC GAAGTGAAG GACGGATACA CTTGATCTC 780
TATCCTGTGA TAAGACGGAC GATAAACCTG CCACATACA CGCTTGAGGC CGTTTATGAA 840
GCCGTCTTCG GTCAGCCGAA GGAGAAAGTT TACGCTGAGG AAATAACCAC AGCCTGGGAA 900
ACCGGCGAGA ACCTTGAGAG AGTCGCCCGC TACTCGATGG AAGATGCGAA GGTACATAC 960
GAGCTTGGGA AGGAGTTCTT TCCGATGGAG GCCCAGCTTT CTCGCTTAAT CGGCCAGTCC 1020
CTCTGGGACG TCTCCCGCTC CAGCACTGGC AACCTCGTG AGTGGTTCCT CCTCAGGAAG 1080
GCCTATGAGA GGAATGAGCT GGCCCCGAAC AAGCCCGATG AAAAGGAGCT GGCCAGAAGA 1140
CGGCAGAGCT ATGAAGGAGG CTATGTAAAA GAGCCCGAGA GAGGTTGTG GGAGAACATA 1200
GTGTACCTAG ATTTTAGATC CCTGTACCCC CTCAATCATCA TCACCCACAA CGTCTCGCCG 1260
GATACGCTCA ACAGAGAAGG ATGCAAGGAA TATGACGTTG CCCACAGGT CGGCCACCGC 1320
TTCTGCAAGG ACTTCCCAGG ATTTATCCCG AGCCTGCTTG GAGACCTCCT AGAGGAGAGG 1380
CAGAAGATAA AGAAGAAGAT GAAGGCCACG ATTGACCCGA TCGAGAGGAA GCTCCTCGAT 1440
TACAGGCAGA GGGCCATCAA GATCCTGGCA AACAGCTACT ACGTTACTA CGGCTATGCA 1500
AGGGCGCGCT GGTA CTGCAA GGAGTGTGCA GAGAGCGTAA CGGCCGTGGG AAGGGAGTAC 1560
ATAACGATGA CCATCAAAGGA GATAGAGGAA AAGTACGGCT TTAAGGTAAT CTACAGCGAC 1620
ACCGACGGAT TTTTGGCCAC AATACCTGGA GCCGATGCTG AAACCGTCAA AAAGAAGGCT 1680
ATGGAGTTCC TCAAGTATAT CAACGCCAAA CTTCGGGCG CGCTTGAGCT CGAGTACGAG 1740
GGCTTCTACA AACGGGCTT CTTCGTCACG AAGAAGAGT ATGCGGTGAT AGACGAGGAA 1800
GGCAAGATAA CAACGCGCGG ACTTGAGATT GTGAGCGTG ACTGGAGCGA GATAGCGAAA 1860
GAGACGCAGG CGAGGGTTCT TGAAGCTTTG CTAAAGGACG GTGACGTCA GAAGGCCGTG 1920
AGGATAGTCA AGAAGTTAC CGAAAAGCTG AGCAAGTACG AGGTTCCGCC GGAGAAAGCTG 1980
GTGATCCACG AGCAGATAAC GAGGGATTTA AAGGACTACA AGGCAACCGG TCCCCACGTT 2040
GCCGTTGCCA AGAGTTGGC CGCGAGAGGA GTCAAAATAC GCCCTGGAAC GGTGATAAGC 2100
TACATCGTGC TCAAGGGCTC TGGGAGGATA GGCGACAGGG CGATACCGTT CGACGAGTTC 2160
GACCCGACGA AGCACAAGTA CGACGCCGAG TACTACATTG AGAACAGGT TCTCCAGCC 2220
GTTGAGAGAA TTCTGAGAGC CTTCCGGTTAC CGCAAGGAAG ACCTGCGCTA CCAGAAGACG 2280
AGACAGGTTG GTTTGAGTGC TTGGCTGAAG CCGAAGGGAA CT //TAG 2325

Figure 17GG

Replacement

Figure

(PCNA) -Vent DNA POLYMERASE FUSION PROTEIN

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 35)

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 36)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC	54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA	108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG	162
TCA AGC ATA TTT AGC AAA TAT GAA GTT GTT GAA CCA GAA ACA ATT GGA GTT AAC	216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA	270
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA	324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA	378
GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT	432
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT	486
GAA TTT ATA ATG AAG GCA GAG GGA GAA ACC CAG GAA GTT GAG ATA AAG CTA ACT	540
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA	594
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA	648
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA	702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG //	

ATGATACTGG ACACTGATTA CATAACAAA GATGGCAAGC CTATAATCCG AATTTTAAAG	60
AAAGAGAACG GGGAGTTTAA AATAGAACTT GACCCTCATT TTCAGCCCCA TATATATGCT	120
CTTCTCAAAG ATGACTCCGC TATTGAGGAG ATAAAGGCAA TAAAGGGCGA GAGACATGGA	180
AAAACGTGTA GAGTGCTCGA TGCAGTGAAA GTCAGGAAAA AATTTTGGG AAGGGAAGTT	240
GAAGTCTGGA AGCTCATTTT CGAGCATCCC CAAGACXXXC CAGCTATGCG GGCACAAATA	300
AGGGAACATC CAGCTGTGGT TGACATTTAC GAATATGACA TACCCTTTGC CAAGCGTTAT	360
CTCATAGACA AGGCCTTGAT TCCCATGGAG GGAGACGAGG AGCTTAAGCT CCTTGCCTTT	420
GATATTGAAA CGTTTATCA TGAGGGAGAT GAATTGGAA AGGCGAGAT AATAATGATT	480
AGTTATGCCG ATGAAGAAGA GGCCAGAGTA ATCACATGGA AAAATATCGA TTTGCCGTAT	540
GTCGATGTTG TGTCCAATGA AAGAGAAATG ATAAAGCGTT TTGTTCAAGT TGTAAAGAA	600
AAAGACCCCG ATGTGATAAT AACTTACAAT GGGACAATT TTGATTGGCC GTATCTCATA	660
AAACGGGCAG AAAAGCTGGG AGTTCGGCTT GTCTTAGGAA GGCACAAAGA ACATCCCGAA	720

Replacement

Figure

CCCAAGATTC AGAGGATGGG TGATAGTTTT GCTGTGAAA TCAAGGGTAG AATCCACTTT 780
GATCTTTTCC CAGTTGTGCG AAGGACGATA AACCTCCCAA CGTATACGCT TGAGGCAGTT 840
TATGAAGCAG TTTTAGGAAA AACCAAAAGC AAATTAGGAG CAGAGGAAAT TGCCGCTATA 900
TGGGAAACAG AAGAAAGCAT GAAAAACTA GCCCAGTACT CAATGGAAGA TGCTAGGGCA 960
ACGTATGAGC TCGGGAAGGA ATTCTTCCCC ATGGAAGCTG AGCTGGCAAA GCTGATAGGT 1020
CAAAGTGAT GGGACGTCTC GAGATCAAGC ACCGGCAACC TCGTGGAGTG GTATCTTTTA 1080
AGGGTGGCAT ACGCGAGGAA TGAAC TTGCA CCGAACAAAC CTGATGAGGA AGAGTATAAA 1140
CGGCGCTTAA GAACAACCTTA CCTGGGAGGA TATGTAAAAG AGCCAGAAAA AGGTTTGTGG 1200
GAAAAATATCA TTTATTGGA TTTCCGCAGT CTGTACCCTT CAATAATAGT TACTCACAAAC 1260
GTATCCCCAG ATACCCTTGA AAAAGAGGGC TGTAAGAATT ACGATGTTGC TCCGATAGTA 1320
GGATATAGGT TCTGCAAGGA CTTTCCGGGC TTTATTCCCT CCATACTCGG GGACTTAATT 1380
GCAATGAGGC AAGATATAAA GAAGAAAATG AAATCCACAA TTGACCCCGAT CGAAAAAGAAA 1440
ATGCTCGATT ATAGGCAAAG GGCTATTAAA TTGCTTGCAA ACAGCTATTA CGGCTATATG 1500
GGGTATCCTA AGGCAAGATG GTACTCGAAG GAATGTGCTG AAAGCGTTAC CGCATGGGG 1560
AGACACTACA TAGAGATGAC GATAAGAGAA ATAGAGGAAA AGTTCGGCTT TAAGGTTCTT 1620
TATGCGGACA CTGACGGCTT TTA TGCCACA ATACCCGGGG AAAAGCCTGA ACTCATTA 1680
AAGAAAAGCCA AGGAATTCCT AAAC TACATA AACTCCAAAC TTCCAGGTCT GCTTGAGCTT 1740
GAGTATGAGG GCTTTTACTT GAGAGGATTC TTTGTTACAA AAAAGCGCTA TGCAGTCATA 1800
GATGAAGAGG GCAGGATAAC AACAAAGGGC TTGGAAGTAG TAAGGAGAGA TTGGAGTGAG 1860
ATAGCTAAGG AGACTCAGGC AAAGGTTTTA GAGGCTATAC TTAAGAGAGG AAGTGTTGAA 1920
AAAGCTGTAG AAGTTGTTAG AGATGTTGTA GAGAAAATAG CAAAATACAG GGTTCCACTT 1980
GAAAAGCTTG TTATCCATGA GCAGATTACC AGGGATTTAA AGGACTACAA AGCCATTGGC 2040
CCTCATGTG CGATAGCAAA AAGACTTGCC GCAAGAGGGA TAAAAGTGAA ACCGGGCACA 2100
ATAATAAGCT ATATCGTTCT CAAAGGGAGC GGAAGAGATAA GCGATAGGGT AATTTTACTT 2160
ACAGAATACG ATCCTAGAAA ACACAAGTAC GATCCGGACT ACTACATAGA AAACCAAGTT 2220
TTGCCGGCAG TACTTAGGAT ACTCGAAGCG TTTGGATACA GAAAGGAGGA TTTAAGGTAT 2280
CAAAGCTCAA AACAAACCGG CTTAGATGCA TGGCTCAAGA GGTAG 2325

Figure 17HH

Vent DNA POLYMERASE - (PCNA) FUSION PROTEIN

Replacement

Figure

Nucleotide sequence (SEQ ID NO: 35) // Nucleotide sequence (SEQ ID NO: 67)
Nucleotide sequence (SEQ ID NO: 36) // Nucleotide sequence (SEQ ID NO: 67)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATACTGG ACACTGATTA CATAACAAAA GATGGCAAGC CTATAATCCG AATTTTAAAG 60
AAAGAGAACG GGGAGTTTAA AATAGAACTT GACCCTCATT TTCAGCCCTA TATATATGCT 120
CTTCTCAAAG ATGACTCCGC TATTGAGGAG ATAAAGGCAA TAAAGGGCGA GAGACATGGA 180
AAAAC TGTA GAGTGCTCGA TGCAGTGAAA GTCAGGAAAA AATTTTGGG AAGGGAAGTT 240
GAA GTCTGGA AGCTCATTTT CGAGCATCCC CAAGACXXXC CAGCTATGCG GGCACAAAATA 300
AGGGAACATC CAGCTGTGGT TGACATTTAC GAATATGACA TACCCTTTGC CAAGCGTTAT 360
CTCATAGACA AGGGCTTGAT TCCCATGGAG GGAGACGAGG AGCTTAAGCT CCTTGCCTTT 420
GATATTGAAA CGTTTTATCA TGAGGGAGAT GAATTTGGAA AGGGCGAGAT AATAATGATT 480
AGTTATGCCG ATGAAGAAGA GGCCAGAGTA ATCACATGGA AAAATATCGA TTTGCCGTAT 540
GTCGATGTTG TGTCCAATGA AAGAGAAATG ATAAAGCGTT TTGTTCAAAGT TGTTAAAGAA 600
AAAGACCCCG ATGTGATAAT AACTTACAAT GGGACAAATT TTGATTTGCC GTATCTCATA 660
AAACGGGCAG AAAAGCTGGG AGTTCGGCTT GTCTTAGGAA GGGACAAAGA ACATCCCCGAA 720
CCCAAGATTG AGAGGATGGG TGATAGTTT GCTGTGAAA TCAAGGGTAG AATCCACTTT 780
GATCTTTTCC CAGTTGTGCG AAGGACGATA AACCTCCCAA CGTATACGCT TGAGGCAGTT 840
TATGAAAGCAG TTTTAGGAAA AACCAAAGC AAATTAGGAG CAGAGGAAAT TGCCGCTATA 900
TGGGAAACAG AAGAAAGCAT GAAAAAATA GCCCAGTACT CAATGGAAGA TGCTAGGGCA 960
ACGTATGAGC TCGGGAAGGA ATTCTTCCCC ATGGAAGCTG AGCTGGCAA GCTGATAGGT 1020
CAAAGTGAT GGGACGTCTC GAGATCAAGC ACCGGCAACC TCGTGGAGTG GTATCTTTTA 1080
AGGGTGGCAT ACGCGAGGAA TGAAC TTGCA CCGAACAAAC CTGATGAGGA AGAGTATAAA 1140
CGGCGCTTAA GAACAAC TTA CCTGGGAGGA TATGTAAAAG AGCCAGAAAA AGGTTTGTGG 1200
GAAAATATCA TTTATTGGA TTTCCGCAGT CTGTACCCTT CAATAATAGT TACTCACAAAC 1260
GTATCCCCAG ATACCCTTGA AAAAGAGGGC TGTAAGAAAT ACGATGTTGC TCCGATAGTA 1320
GGATATAGGT TCTGCAAGGA CTTTCCGGGC TTTATTCCCT CCATACTCGG GGACTTAAT 1380
GCAATGAGGC AAGATATAAA GAAGAAAATG AAATCCACAA TTGACCCGAT CGAAAAAGAA 1440
ATGCTCGATT ATAGGCAAAG GGCTATTAAA TTGCTTGCAA ACAGCTATTA CGGCTATATG 1500
GGGTATCCTA AGGCAAGATG GTACTCGAAG GAATGTGCTG AAAGCGTTAC CGCATGGGG 1560
AGACACTACA TAGAGATGAC GATAAGAGAA ATAGAGGAAA AGTTCGGCTT TAAGGTTCTT 1620
TATGCGGACA CTGACGGCTT TTATGCCACA ATACCCGGG AAAAGCCTGA ACTCATTA 1680
AAGAAAAGCCA AGGAATTCCT AAAC TACATA AACTCCAAAC TTCCAGGTCT GCTTGAGCTT 1740
GAGTATGAGG GCTTTTACTT GAGAGGATTC TTTGTTACAA AAAAGCGCTA TGCAGTCATA 1800

Replacement

Figure

GATGAAGAGG	GCAGGATAAC	AACAAGGGGC	TTGGAAGTAG	TAAGGAGAGA	TTGGAGTGAG	1860
ATAGCTAAGG	AGACTCAGGC	AAAGGTTTTA	GAGGCTATAC	TTAAAGAGGG	AAGTGTTGAA	1920
AAAGCTGTAG	AAGTTGTTAG	AGATGTTGTA	GAGAAAATAG	CAAAATACAG	GGTTCACACTT	1980
GAAAAGCTTG	TTATCCATGA	GCAGATTACC	AGGGATTTAA	AGGACTACAA	AGCCATTGGC	2040
CCTCATGTCC	CGATAGCAAA	AAGACTTGCC	GCAAGAGGGA	TAAAAGTGAA	ACCGGGCACA	2100
ATAATAAGCT	ATATCGTTCT	CAAAAGGGAGC	GGAAAGATAA	CGGATAGGGT	AATTTTACTT	2160
ACAGAAATACG	ATCCTAGAAA	ACACAAGTAC	GATCCGGACT	ACTACATAGA	AAACCAAGTT	2220
TTGCCGGCAG	TACTTAGGAT	ACTCGAAGCG	TTTGGATACA	GAAAGGAGGA	TTTAAAGGTAT	2280
CAAAGCTCAA	AACAAACCGG	CTTAGATGCA	TGGCTCAAGA	GG 2325	//	

ATG CCA	TTT GAA	ATC GTA	TTT GAA	GGT GCA	AAA GAG	TTT GCC	CAA CTT	ATA GAC	54
ACC GCA	AGT AAG	TTA ATA	GAT GAG	GCC GCG	TTT AAA	GTT ACA	GAA GAT	GGG ATA	108
AGC ATG	AGG GCC	ATG GAT	CCA AGT	AGA GGT	GTC ATT	GAC CTA	AAT CTC	CCG	162
TCA AGC	ATA TTT	AGC AAA	TAT GAA	GTT GAA	CCA GAA	ACA ATT	GGA GTT	AAC	216
ATG GAC	CAC CTA	AAG AAG	ATC CTA	AAG AGA	GGT AAA	GCA AAG	GAC ACC	TTA ATA	270
CTC AAG	AAA GGA	GAG GAA	AAC TTC	TTA GAG	ATA ACA	ATT CAA	GGA ACT	GCA ACA	324
AGA ACA	TTT AGA	GAT GGT	CCC CTA	ATA GAT	GTA GAA	ATG GAA	GTT GAC	CTC CCA	378
GAA CTT	CCA TTC	ACT ACT	GCA AAG	GTT GTA	GTT CTT	GGA GAA	GTC CTA	AAA GAT	432
GTT AAA	GAT GCC	TCT CTA	GTG AGT	GAC AGC	ATA AAA	TTT ATT	GCC AGG	GAA AAT	486
GAA TTT	ATA ATG	AAG GCA	GAG GGA	GAA ACC	CAG GAA	GTT GAG	ATA AAG	CTA ACT	540
CTT GAA	GAT GAG	GGA TTA	TTG GAC	ATC GAG	GTT CAA	GAG GAG	ACA AAG	AGC GCA	594
TAT GGA	GTC AGC	TAT CTC	TCC GAC	ATG GAT	AAA GGA	CTT GGA	AAG GCC	GAT GAA	648
GTT ACA	ATA AAG	TTT GGA	AAT GAA	ATG CCC	ATG CAA	ATG GAG	TAT TAC	ATT AGA	702
GAT GAA	GGA AGA	CTT ACA	TTC CTA	CTG GCT	CCA AGA	GTT GAA	GAG TGA		

Figure 17II

Deep Vent- (PCNA) DNA polymerase fusion protein

Replacement

Figure

Nucleotide sequence (SEQ ID NO: 37) // Nucleotide sequence (SEQ ID NO: 67)
Nucleotide sequence (SEQ ID NO: 38) // Nucleotide sequence (SEQ ID NO: 67)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
ATGATACTTG ACGCTGACTA CATCACCGAG GATGGGAAGC CGATTATAAG GATTTTCAAG 60
AAAGAAAACG GCGAGTTTAA GGTGAGTAC GACAGAAACT TTAGACCTTA CATTTACGCT 120
CTCCTCAAAG ATGACTCGCA GATTGATGAG GTTAGGAAGA TAACCGCCGA GAGGCATGGG 180
AAGATAGTGA GAATTATAGA TGCCGAAAAG GTAAGGAAGA AGTTCTTGGG GAGGCCGATT 240
GAGGTATGGA GGCTGTACTT TGAACACCCCT CAGGACXXXC CCGCAATAAG GGATAAGATA 300
AGAGAGCATT CCGCAGTTAT TGACATCTTT GAGTACGACA TTCCGTTTCG GAAAGAGGTAC 360
CTAATAGACA AAGGCCTAAT TCCAATGGAA GCGGATGAAG AGCTCAAGTT GCTCGCATTT 420
GACATAGAAA CCTCTATCA CGAAGGGGAG GAGTTCGCGA AGGGCCCCAT TATAATGATA 480
AGCTATGCTG ATGAGGAAGA AGCCAAAGTC ATAACTGGA AAAAGATCGA TCTCCCCGTAC 540
GTCGAGGTAG TTTCCAGCGA GAGGGAGATG ATAAAGCGGT TCCTCAAGGT GATAAGGGAG 600
AAAGATCCCG ATGTTATAAT TACCTACAAC GCGATTCTT TCGACCTTCC CTATCTAGTT 660
AAGAGGCCCG AAAAGCTCGG GATAAAGCTA CCCCTGGGAA GGGACGGTAG TGAGCCAAAG 720
ATGCAGAGGC TTGGGGATAT GACAGCGGTG GAGATAAAGG GAAGGATACA CTTTGACCTC 780
TACCACGTGA TTAGGAGAAC GATAAACCTC CCAACATACA CCCTCGAGGC AGTTTATGAG 840
GCAATCTTCG GAAAGCCAAA GGAGAAAAGTT TACGCTCACG AGATAGCTGA GGCCTGGGAG 900
ACTGGAAAGG GACTGGAGAG AGTTGCAAG GCCCAGCTTT CAAGGTTAGT CGGCCAGCCC 960
GAGCTCGGTA GGGAGTTCTT CCCAATGGAG GACTGCAAGT AGGTTAGT CCGCCAGCCC 1020
CTGTGGGATG TTTCTAGGTC TTCAACTGGC AACTTGGTGG AGTGGTACCT CCTCAGGAAG 1080
GCCTACGAGA GGAATGAATT GGCTCCAAAC AAGCCGGATG AGAGGGAGTA CGAGAGAAGG 1140
CTAAGGGAGA GCTACGCTGG GGGATACGTT AAGGAGCCGG AGAAAAGGCT CTGGGAGGGG 1200
TTAGTTTCCC TAGATTTCAG GAGCCTGTAC AGGGTGTAGG GAATACGATA TAACGTCTCA 1260
CCGATACGC TGAACAGGGA AGGGTGTAGG GAATACGATG TCGCCCCAGA GGTGGGCAC 1320
AAGTTCTGCA AGGACTTCCC GGGGTTTATC CCAGCCTGC TCAAGAGGTT ATTGGATGAA 1380
AGGCAAGAAA TAAAAGGAA GATGAAAGCT TCTAAAGACC CAATCGAGAA GAAGATGCTT 1440
GATTACAGGC AACGGGCAAT CAAAATCCTG GCAAAACAGCT ATTATGGTA TTATGGGTAC 1500
GCAAAAAGCCC GTTGGTACTG TAAGGAGTGC GCAGAGAGCG TTACGGCCTG GGGAGGGAA 1560
TATATAGAGT TCGTAAGGAA GGAACCTGGAG GAAAAGTTCTG GGTTCAAAAGT CTTATACATA 1620
GACACAGATG GACTCTACGC CACAATTCTT GGGGCAAAAC CCGAGGAGAT AAAGAAGAAA 1680
GCCCTAGAGT TCGTAGATTA TATAACGCC AAGCTCCCAG GGCTGTTGGA GCTTGAGTAC 1740
GAGGGCTTCT ACGTGAGAGG GTTCTTTCGTG ACGAAGAAGA AGTATGCGTT GATAGATGAG 1800
GAAGGGAAGA TAATCACTAG GGGGCTTGAA ATAGTCAGGA GGGACTGGAG CGAAATAGCC 1860

Replacement

Figure

AAAGAAACCC AAGCAAAAGT CCTAGAGGCT ATCCTAAAGC ATGGCAACGT TGAGGAGGCA 1920
GTAAAGATAG TTAAGGAGGT AACTGAAAAG CTGAGCAAGT ACGAAATACC TCCAGAAAAG 1980
CTAGTTATTT ACGAGCAGAT CACGAGGCC CTTACAGAGT ACAAGGCTAT AGTCCGCAC 2040
GTTGCCGTGG CAAAAAGGTT AGCCGCTAGA GGAGTAAAGG TGAGGCCCTGG CATGGTGATA 2100
GGGTACATAG TGCTGAGGG AGACGGGCCA ATAAGCAAGA GGGCTATCCT TGCAGAGGAG 2160
TTCGATCTCA GGAAGCATAA GTATGACGCT GAGTATTACA TAGAAAATCA GGTTTTACCT 2220
GCCGTTCTTA GAATATTAGA GGCCTTTGGG TACAGGAAAG AAGACCTCAG GTGGCAGAAG 2280
ACTAAACAGA CAGGTCTTAC GGCATGGCTT AACATCAAGA AGAAG // 2328

ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC 54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA 108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG 162
TCA AGC ATA TTT AGC AAA TAT GAA GTT GTT GAA CCA GAA ACA ATT GGA GTT AAC 216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA 270
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA 324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA 378
GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT 432
GTT AAA GAT GCC TCT CTA GTG AGT GAG GAA ACC CAG GAA GTT GAG ATA AAG CTA ACT 486
GAA TTT ATA ATG AAG GCA GAG GGA GAA ACC CAG GAA GTT GAG ATA AAG CTA ACT 540
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA 594
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA 648
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA 702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG TGA

Figure 17JJ

(PCNA) - Deep Vent DNA polymerase fusion protein

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 37)

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 38)

Replacement

Figure

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC	54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA	108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG	162
TCA AGC ATA TTT AGC AAA TAT GAA GTT GTT GAA CCA GAA ACA ATT GGA GTT AAC	216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA	270
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA	324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA	378
GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT	432
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT	486
GAA TTT ATA ATG AAG GCA GAG GGA ACC CAG GAA GTT GAG ATA AAG CTA ACT	540
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA	594
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA	648
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA	702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG //	

ATGATACTTG ACGCTGACTA CATCACCAGG GATGGGAAGC CGATTATAAG GATTTTCAAG	60
AAAGAAACG GCGAGTTTAA GGTGAGTAC GACAGAAACT TTAGACCTTA CATTTACGCT	120
CTCCTCAAAG ATGACTCGCA GATTGATGAG GTTAGGAAGA TAACCGCCGA GAGGCATGGG	180
AAGATAGTGA GAATTATAGA TGCCGAAAG GTAAGGAAGA AGTTCTCTGG GAGGCCGATT	240
GAGGTATGGA GGCTGTACTT TGAACACCCT CAGGACXXC CCGCAATAAG GGATAAGATA	300
AGAGAGCATT CCGCAGTTAT TGACATCTTT GAGTACGACA TTCCGTTTCG GAAGAGGTAC	360
CTAATAGACA AAGGCCTAAT TCCAATGGAA GCGGATGAAG AGCTCAAGTT GCTCGCATTT	420
GACATAGAAA CCTCTATCA CGAAGGGGAG GAGTTCGCGA AGGGCCCCAT TATAATGATA	480
AGCTATGCTG ATGAGGAAGA AGCCAAAGTC ATAACGTGGA AAAAGATCGA TCTCCCGTAC	540
GTCGAGGTAG TTTCCAGCGA GAGGGAGATG ATAAAGCGGT TCCTCAAGGT GATAAGGGAG	600
AAAGATCCC ATGTTATAAT TACCTACAAC GCGATTCTT TCGACCTTCC CTATCTAGTT	660
AAGAGGGCCG AAAAGCTCGG GATAAAGCTA CCCCTGGGAA GGGACGGTAG TGAGCCAAAG	720
ATGCAGAGGC TTGGGGATAT GACAGCGGTG GAGATAAAGG GAAGGATACA CTTTGACCTC	780
TACCACGTGA TTAGGAGAAC GATAAACCTC CCAACATACA CCCTCGAGGC AGTTTATGAG	840
GCAATCTTCG GAAAGCCAAA GGAGAAAGTT TACGCTCAG AGATAGCTGA GGCCTGGAG	900
ACTGGAAAGG GACTGGAGAG AGTTGCAAG TATTCAATGG AGGATGCAAA GGTAACGTAC	960
GAGCTCGGTA GGGAGTTCTT CCCAATGGAG GCCCAGCTTT CAAGGTTAGT CGGCCAGCCC	1020

Replacement

Figure

CTGTGGGATG	TTTCTAGGTC	TTCAACTGGC	AACTTGGTGG	AGTGGTACCT	CCTCAGGAAG	1080
GCCTACGAGA	GGAATGAATT	GGCTCCAAAC	AAGCCGGATG	AGAGGGAGTA	CGAGAGAAGG	1140
CTAAGGGAGA	GCTACGCTGG	GGGATACGTT	AAGGAGCCGG	AGAAAGGGCT	CTGGGAGGGG	1200
TTAGTTTCCC	TAGATTTCAG	GAGCCTGTAC	CCCTCGATAA	TAATCACCCA	TAACGTCTCA	1260
CCGGATACGC	TGAACAGGGA	AGGGTGTAGG	GAATACGATG	TCGCCCCAGA	GGTTGGGCAC	1320
AAGTTCTGCA	AGGACTTCCC	GGGGTTTATC	CCCAGCCTGC	TCAAGAGGTT	ATTGGATGAA	1380
AGGCAAGAAA	TAAAAAGGAA	GATGAAAGCT	TCTAAAGACC	CAATCGAGAA	GAAGATGCTT	1440
GATTACAGGC	AACGGGCAAT	CAAAATCCTG	GCAACACAGCT	ATTATGGGTA	TTATGGGTAC	1500
GCAAAAAGCCC	GTTGGTACTG	TAAGGAGTGC	GCAGAGAGCG	TTACGGCCTG	GGGAGGGGAA	1560
TATATAGAGT	TCGTAAAGGAA	GAAACTGGAG	GAAAAGTTCTG	GGTTCAAAAGT	CTTATACATA	1620
GACACAGATG	GACTCTACGC	CACAATTCTT	GGGGCAAAAC	CCGAGGAGAT	AAAGAAGAAA	1680
GCCCTAGAGT	TCGTAGATTTA	TATAAACGCC	AAGCTCCCAG	GGCTGTTGGA	GCTTGAGTAC	1740
GAGGGCTTCT	ACGTGAGAGG	GTTCTTTCGTG	ACGAAGAAGA	AGTATGCGTT	GATAGATGAG	1800
GAAAGGGAAGA	TAATCACTAG	GGGGCTTGAA	ATAGTCAGGA	GGGACTGGAG	CGAAATAGCC	1860
AAAGAAACCC	AAGCAAAAGT	CCTAGAGGCT	ATCCTAAAGC	ATGGCAACGT	TGAGGAGGCA	1920
GTAAAGATAG	TTAAGGAGGT	AAC TGAAAG	CTGAGCAAGT	ACGAAATACC	TCCAGAAAAAG	1980
CTAGTTATTT	ACGAGCAGAT	CACGAGGCC	CTTCACGAGT	ACAAGGCTAT	AGGTCCGCAC	2040
GTTGCCCGTGG	CAAAAAGGTT	AGCCGCTAGA	GGAGTAAAGG	TGAGGCCTGG	CATGGTGATA	2100
GGGTACATAG	TGCTGAGGGG	AGACGGGCCA	ATAAGCAAGA	GGCTATCCT	TGCAGAGGAG	2160
TTCGATCTCA	GGAAGCATAA	GTATGACGCT	GAGTATTACA	TAGAAAAATCA	GGTTTTACCT	2220
GCCGTTCTTA	GAATATTAGA	GGCCTTTGGG	TACAGGAAAG	AAGACCTCAG	GTGGCAGAAG	2280
ACTAAACAGA	CAGGTCTTAC	GGCATGGCTT	AACATCAAGA	AGAAG TAA		2328

Figure 17KK

JDF-3 - (PCNA) fusion protein

Nucleotide sequence (SEQ ID NO: 39) // Nucleotide sequence (SEQ ID NO: 67)
Nucleotide sequence (SEQ ID NO: 40) // Nucleotide sequence (SEQ ID NO: 67)

Replacement

Figure

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATCCTTGACGTTGATTACATCACCGAGAATGGAAGCCCGTCATCAGGGTCTTCAAGAAGGAGAACGGCGAGTTCAGGATTGAATACGACCGGAGTTCGAGCCCTACTTCT
ACGGCTCCTCAGGGACGACTCTGCCATCGAAGAAATCAAAAGATAAACCGGAGAGCACGGCAGGTCGTTAAGGTTAAGCGCGGAGAAAGTGAAGAAAAGTTCCCTCGG
CAGGTCTGTGGAGGTCCTGGTCCCTACTTCACGCACCCCGCAGGACXXXCCGCAATCCCGACAAAATAAGGAAGCACCCCGGTCAATCGACATCTACGAGTACGACATACCC
TTCGCCAAGCGCTACCTCATAGACAAGGGCCTAATCCCGATGGAAGGTGAGGAAGAGCTTAAACTCATGTCTTTCGACATCGAGACGCTCTACCCAGGAGAAAGAGTTTGGAA
CCGGCCGATTCTGATGATAAGCTACGCCGATGAAGCGGCGGTGATAAACCTGGAAGAAGATCGACCTTCTTACGTTGAGGTTGTCTCCACCGAGAAAGGAGATGATTAA
GCGCTTCTTGAGGTCGTTAAGGAGAGACCCGACGTCGTGATAACATACAAACGGCACAACCTTCGACTTCGCCCTACCTGAAAAGCGCTGTGAGAAAGCTTTGGCGTGAGCTTT
ACCTCGGGAGGACGGGAGCGAGCCGAAGATACAGCGCATGGGGACAGGTTTGCGGTGAGGTGAAGGCAGGTACACTTCGACCTTTATCCAGTCATAAGCGCACCATAA
ACCTCCGACCTACACCTTGAGGCTGTATACGAGGCGGTTTTCGGCAAGCCCAAGGAGAGGTCTACGCCGAGGAGATAGCCACCGCTGGGAGACCGGCGAGGGCTTGAGAG
GGTCGCGCTACTCGATGGAGGACCGGAGGTTACCTACGAGCTTGGCAGGAGTTCTTCCGATGGAGGCCAGCTTTCAGGCTCATCGGCCAAGCCTCTGCGGACGTTTCC
CGCTCCAGCACCGGCAACCTCGTCGAGTGTTCTCTTAAGGAAGCCCTACGAGAGGAACGAACTCGCTCCCAACAAGCCCGACGAGAGGAGCTGGCGAGGAGAAAGGGGGCT
ACGCCGTGGCTACGTCAAGGAGCGGAGCGGGACTGTGGACAATATCGTGATCTAGACTTTCGTAGTCTCTACCTTCAATCATATACCCACAACGCTCTCGCCAGATAC
GCTCAACCGGAGGGGTGAGGAGCTACGACGTTGCCCGGAGGTCTGTCAAGGACTTCCCGGCTTCATTCGGAGCCTGCTCGGAAACCTGCTGGAGGAAAGG
CAGAAGATAAAGAGGAAGATGAAGGCAACTCTCGACCCGCTGGAGAAGAAATCTCCTCGATTACAGGCAACCGGCCATCAAGATTCTCGCCAACAGCTACTACGGCTACGGCT
ATGCCAGGGCAAGATGGTACTGCGAGGAGTGCGCGAGAGCGTTACGGCATGGGGAAGGGAGTACATCGAAATGGTCAATCAGAGAGCTTGAGGAAAGTTTCGGTTTAAAGTCCT
CTATGCAGACACAGACGCTCTCCATGCCACCATTCCTGGAGCGGACGCTGAACACAGTCAAGAAAAGGCAATGGAGTTCTTAAACTATATCAATCCCAAACTGCCCGCTCTC
GAACTCGAATACGAGGGCTTCTACGTCAGGGGCTTCTTCGTACGAAGAAAAGTACGCGGTCAATCGACGAGAGGGCAAGATAACACGCGGGCTTGAGATAGTCAGGCGCG
ACTGGAGCGAGATAGCGAAGGAGACGCGGAGGGTTTTGAGGCGATACTCAGGCACGGTGACGTTGAAGAGGCCGTCAGAAATTGTCAGGGAAGTCACCGAAAAGCTGAGCAA
GTACGAGGTTCCGCCGGAGAAAGCTGGTTATCCACGAGCAGATAACGCGGAGCTCAAGGACTACAAGCCACCGGCCGACGTAGCCATAGCGAAGcGTTTGGCCGCCAGAGGT
GTTAAATCCGGCCCGAACTGTGATAAGCTACATCGTTCTGAAGGCTCCGGAAGGATAGGCGACAGGGCGATTCCCTTCGACGAGTTTCGACCCGACGAAAGCACAAGTACGATG
CGGACTACTACATCGAGAACCAAGGTTCTGCCGCGAGTTGAGAGAATCCTCAGGGCTTCGGCTACCGCAAGGAAGACCTGCGCTACCAGAAGACGAGGCGAGGCTTGGCGC
GTGGCTGAAGCCGAAGGGGAAGAAG//

ATG	CCA	TTT	GAA	ATC	GTA	TTT	GAA	GGT	GCA	AAA	GAG	TTT	GCC	CAA	CTT	ATA	GAC	54
ACC	GCA	AGT	AAG	TTA	ATA	GAT	GAG	GCC	GCG	TTT	AAA	GTT	ACA	GAA	GAT	GGG	ATA	108
AGC	ATG	AGG	GCC	ATG	GAT	CCA	AGT	AGA	GTT	GTC	CTG	ATT	GAC	CTA	AAT	CTC	CCG	162
TCA	AGC	ATA	TTT	AGC	AAA	TAT	GAA	GTT	GAA	CCA	GAA	ACA	ATT	GGA	GTT	AAC		216
ATG	GAC	CAC	CTA	AAG	AAG	ATC	CTA	AAG	AGA	GGT	AAA	GCA	AAG	GAC	ACC	TTA	ATA	270
CTC	AAG	AAA	GGA	GAG	GAA	AAC	TTC	TTA	GAG	ATA	ACA	ATT	CAA	GGA	ACT	GCA	ACA	324
AGA	ACA	TTT	AGA	GTT	CCC	CTA	ATA	GAT	GTA	GAA	GAG	ATG	GAA	GTT	GAC	CTC	CCA	378
GAA	CTT	CCA	TTC	ACT	GCA	AAG	GTT	GTA	GTT	CTT	GGA	GAA	GTC	CTA	AAA	GAT	GCT	432
GTT	AAA	GAT	GCC	TCT	CTA	GTG	AGT	GAC	AGC	ATA	AAA	TTT	ATT	GCC	AGG	GAA	AAT	486
GAA	TTT	ATA	ATG	AAG	GCA	GAG	GGA	ACC	CAG	GAA	GTT	GAG	ATA	AAG	CTA	ACT		540
CTT	GAA	GAT	GAG	GGA	TTA	TTG	GAC	ATC	GAG	GTT	CAA	GAG	ACA	AAG	AGC	GCA		594
TAT	GGA	GTC	AGC	TAT	CTC	TCC	GAC	ATG	GTT	AAA	GGA	CTT	GGA	AAG	GCC	GAT	GAA	648

Replacement

Figure

GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA 702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG TGA

Figure 17LL

(PCNA) - JDF-3 fusion protein

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 39)

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 40)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC	54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA	108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG	162
TCA AGC ATA TTT AGC AAA TAT GAA GGT GAA CCA GAA ACA ATT GGA GTT AAC	216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA	270
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA	324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA	378
GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT GGA GAA GTC CTA AAA GAT GCT	432
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT	486
GAA TTT ATA ATG AAG GCA GAG GGA GAA ACC CAG GAA GTT GAG ATA AAG CTA ACT	540
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GAA GTT CAA GAG ACA AAG AGC GCA	594
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA	648
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA	702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG //	

ATGATCCTTGACGTTGATTACATCACCGAGAAATGGAAGCCCGTCATCAGGGTCTTCAAGAGGAGAACGGCGAGTTCAGGATTGAATACGACCGGAGTTCGAGCC
CTACTTCTACGCGCTCCTCAGGGACGACTCTGCCATCGAAGAAATCAAAAAGATACCGGGAGAGGCACGGCAGGTCGTTAAGGTTAAGCGCGGAGAAAGTGA
AGAAAAAGTTCCTCGCAGGTCTGTGAGGTCTGGGTCTCTACTTCACGCACCCGACGACXXXCXCGGCAATCCGCGACAAAAATAAGGAAGCACCCCGGTCATC
GACATCTACGAGTACGACATACCTTCGCCAAGCGCTACCTCATAGACAAGGGCCCTAATCCCGATGGAAAGGTGAGGAAGCTTAAACTCATGTCTTQGAQATCQGA
ACGCTCTACCAAGGAGGAGAGAGTTTGGAAACCGGCCGATTCTGATGATAAGCTACGCCGATGAAGCCGAGCGCGCTGATAACCTGGAAGAAGATCGACCTTC

Replacement

Figure

CTTACGTTGAGGTTGTCTCCACCGAGAAAGGAGATGATTAAGCGCTTCTTGAGGGTCGTTAAGGAGAAGGACCCGGACGTGCTGATAACATACAACGGCGACAACCTTC
GACTTCGCCCTACCTGAATAAGCGCTGTGAGAAAGCTTTGGCGTGAGCTTTTACCCCTCGGAGGACGGGAGCCGAAGATACAGCGCATGGGGACAGGTTTGCGGT
CGAGGTGAAGGCAGGGTACACTTCGACCTTTATCCAGTCAATAGCGCACCATAAACCTCCCGACCTACACCCCTTGAGGCTGTATACGAGCGGTTTTCGGCAAGC
CCAAGGAGAAGTCTACGCCGAGGAGATAGCCACCGCTGGGAGACCGCGAGGGCTTGAGAGGGTCCGCGCTACTCGATGGAGGACGCGAGGTTACTCTACGAG
CTTGGCAGGGAGTTCTTCCCAGATGGAGGCCCAGCTTTCAGGCTCATCGGCCAAGGCCCTCTGGGACGTTTCCCGCTCCAGCACCGCAACCTCGTCGAGTGGTTCCT
CCTAAGGAAGGCTACGAGAGGAACGAACTCGCTCCCAACAAAGCCGACGAGAGGAGCTGGCGAGGAGAAGGGGGGCTACgCCGTGGCTACGTCAAGGAGCCGG
AGCGGGGACTGTGGGACAAATATCGTGATCTAGACTTTTCGTAGTCTCTACCCTTCAATCAATAATCACCCACAACGTCTCGCCAGATACGCTCAACCCGAGGGGTGT
AGGAGCTACGACGTTGCCCCGAGGTCGGTCAAAAGTTCTGCAAGGACTTCCCGGCTTCATTCGAGCCTGCTCGGAAACCTGCTGGAGGAAAGGCAGAGATAAA
GAGGAAGATGAAGGCAACTCTCGACCCGCTGGAGAAGAAATCTCTCGATTACAGGCAACGGCCATCAAGATTCTCGCCAACAGCTACTACGGCTACTACGGCTATG
CCAGGGCAAGATGGTACTGCAGGGAGTGCGCCGAGAGCGTTACGGCATGGGGAAGGGAGTACATCGAAATGGTCAATCAGAGAGCTTGAGGAAAAGTTCCGTTTAA
GTCCCTATGCAGACACAGACGGTCTCCATGCCACCATTCCTGGAGCGGACGCTGAACACAGTCAAGAAAAGGCAATGGAGTTCTTAAACTATATCAATCCCAAAC
GCCCCGGCTTCTCGAACTCGAAATACGAGGGCTTCTACGTCAGGGGCTTCTTCGTACGAAAGTAACGCGGTCAATCGACGAGGAGGCAAGATAACCAACGCGG
GGCTTGAGATAGTCAGGCGGACTGGAGCGAGATAGCGAAAGGAGACGACGGCGAGGGTTTGGAGGCGATACTCAGGCACGGTGACGTTGAAAGAGCCGTCAGAAAT
GTCAGGGAAGTCAACGAAAAGCTGAGCAAGTACGAGGTTCCGCCGGAGAGCTGGTTATCCACGAGCAGATAACCGCGGAGCTCAAGGACTACAAGGCCACCGGCCC
GCACGTAGCCATAGCGAAGCGTTTGGCCGCCAGAGGTGTTAAATCCGGCCCCGAACTGTGATAAGCTACATCGTTCTGAAGGCTCCGGAAGGATAGGCGACAGG
CGATTCCCCTTCGACGAGTTCGACCCGACGAAGCACAAAGTACGATGCGGACTACTACATCGAGAACCAAGGTTCTGCGCGGCAGTTGAGAGAAATCCTCAGGGCCTTCGGC
TACCGCAAGGAAGACCTGCGCTACCAAGAAGACGAGGCGAGGTCGGGCTTGGCGCGTGGCTGA

Replacement

Figure

Figure 17MM

Sac7d gene (ACCESSION No: M87569)

Nucleotide sequence (SEQ ID NO: 69)

Amino acid sequence (SEQ ID NO: 70)

M	V	K	K	V	K	F	K	Y	K	G	E	E	K	E	V	D	T	S	18
ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA																			54
K	I	K	K	V	W	R	V	G	K	M	V	S	F	T	T	Y	D	D	36
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC																			108
N	G	K	T	G	R	G	A	V	S	E	K	D	A	P	K	E	L		54
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA																			162
L	D	M	L	A	R	A	E	R	E	K	K	*							67
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA TAA																			201

Figure 17NN

Sac7d-Taq DNA polymerase fusion protein

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 65)

Amino acid sequence (SEQ ID NO: 70) // Amino acid sequence (SEQ ID NO: 66)

M	V	K	V	K	F	K	Y	K	G	E	E	K	E	V	D	T	S	
ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA																		
K	I	K	K	V	W	R	V	G	K	M	V	S	F	T	Y	D	D	
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC																		
N	G	K	T	G	R	G	A	V	S	E	K	D	A	P	K	E	L	
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA																		

Replacement Figure

```

L   D   M   L   A   R   A   E   R   E   K   K   //
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA //

      G   G   G
// GGC GGC GGT

V   T   S   G   M   L   P   L   F   E   P   K   G   R   V   L   L   V
GTC ACT AGT GGG ATG CTG CCC CTC TTT GAG CCC AAG GGC CGG GTC CTC CTG GTG

D   G   H   H   L   A   Y   R   T   F   H   A   L   K   G   L   T   T
GAC GGC CAC CAC CTG GCC TAC CGC ACC TTC CAC GCC CTG AAG GGC CTC ACC ACC

S   R   G   E   P   V   Q   A   V   Y   G   F   A   K   S   L   L   K
AGC CGG GGG GAG CCG GTG CAG GCG GTC TAC GGC TTC GCC AAG AGC CTC CTC AAG

A   L   K   E   D   G   D   A   V   I   V   V   F   D   A   K   A   P
GCC CTC AAG GAG GAC GGG GAC GCG GTG ATC GTG GTC TTT GAC GCC AAG GCC CCC

S   F   R   H   E   A   Y   G   G   G   G   G   TAC AAG GCG GGC CGG GCC ACC GGC CCA

E   D   F   P   R   Q   L   A   L   I   K   E   L   V   D   L   L   G
GAG GAC TTT CCC CGG CAA CTC GCC CTC ATC AAG GAG CTG GTG GAC CTC CTG GGG

L   A   R   L   E   V   P   G   Y   E   A   D   D   V   L   A   S   L
CTG GCG CGC CTC GAG GTC CCG GGC TAC GAG GCG GAC GTC CTG GCC AGC CTG

A   K   K   A   E   K   E   G   Y   E   V   R   I   L   T   A   D   K
GCC AAG AAG GCG GAA AAG GAG GGC TAC GAG GTC CGC ATC CTC ACC GCC GAC AAA

D   L   Y   Q   L   L   S   D   R   I   H   V   L   H   P   E   G   Y
GAC CTT TAC CAG CTC CTT TCC GAC CGC ATC CAC GTC CTC CAC CCC GAG GGG TAC

L   I   T   P   A   W   L   W   E   K   Y   G   L   R   P   D   Q   W
CTC ATC ACC CCG GCC TGG CTT TGG GAA AAG TAC GGC CTG AGG CCC GAC CAG TGG

A   D   Y   R   A   L   T   G   D   E   S   D   N   L   P   G   V   K

```

Replacement Figure

GCC GAC TAC CGG GCC CTG ACC GGG GAC GAG TCC GAC AAC CTT CCC GGG GTC AAG
 G I G E K T A R K L L E E W G S L E
 GGC ATC GGG GAG AAG ACG GCG AGG AAG CTT CTG GAG GAG TGG GGG AGC CTG GAA
 A L L K N L D R L K P A I R E K I L
 GCC CTC CTC AAG AAC CTG GAC CGG CTG AAG CCC GCC ATC CGG GAG AAG ATC CTG
 A H M D D L K L S W D L A K V R T D
 GCC CAC ATG GAC GAT CTG AAG CTC TCC TGG GAC CTG GCC AAG GTG CGC ACC GAC
 L P L E V D F A K R R E P D R E R L
 CTG CCC CTG GAG GTG GAC TTC GCC AAA AGG CGG GAG CCC GAC CGG GAG AGG CTT
 R A F L E R L E F G S L L H E F G L
 AGG GCC TTT CTG GAG AGG CTT GAG TTT GGC AGC CTC CAC GAG TTC GGC CTT
 L E S P K A L E E A P W P P E G A
 CTG GAA AGC CCC AAG GCC CTG GAG GAG GCC CCC TGG CCC CCG GAA GGG GCC
 F V G F V L S R K E P M W A D L L A
 TTC GTG GGC TTT GTG CTT TCC CGC AAG GAG CCC ATG TGG GCC GAT CTT CTG GCC
 L A A A R G G GGC CGG GTC CAC CGG GCC CCC GAG CCT TAT AAA GCC
 CTG GCC GCC AGG GGC CGG CGG GAG GAG GGC CTT CTC GCC AAA GAC CTG AGC GTT CTG
 L R D L K E A R G L L A K D L S V L
 CTC AGG GAC CTG AAG GAG GCG CGG GGG CTT CTC GCC AAA GAC CTG AGC GTT CTG
 A L R E G L G L P P G D D P M L L A
 GCC CTG AGG GAA GGC CTT GGC CTC CCG CCC GGC GAC GAC CCC ATG CTC CTC GCC
 Y L L D P S N T T P E G V A R R Y G
 TAC CTC CTG GAC CCT TCC AAC ACC ACC CCC GAG GGG GTG GCC CGG CGC TAC GGC
 G E W T E E A G E R A A L S E R L F
 GGG GAG TGG ACG GAG GAG GCG GGG GAG CGG GCC CTT TCC GAG AGG CTC TTC

Replacement Figure

A N L L W G R R L E G E E R L L L W L Y R
GCC AAC CTG TGG GGG AGG CTT GAG GGG GAG GAG AGG CTC CTT TGG CTT TAC CGG
E V E R P L S A V L A H M E A T G V
GAG GTG GAG AGG CCC CTT TCC GCT GTC CTG GCC CAC ATG GAG GCC ACG GGG GTG
R L D V A Y L L R A L S L E V A E E I
CGC CTG GAC GTG GCC TAT CTC AGG GCC TTG TCC CTG GAG GTG GCC GAG GAG ATC
A R L E A A E V F R L A G H P F N L N
GCC CGC CTC GAG GCC GAG GTC TTC CGC CTG GCC CAC CCC TTC AAC CTC AAC
S R D Q L E R V L F D E L G L P A I
TCC CGG GAC CAG CTG GAA AGG GTC CTC TTT GAC GAG CTA GGG CTT CCC GCC ATC
G K T E E K T G K R S T S A A V L E A
GGC AAG ACG GAG AAG ACC GGC AAG CGC TCC ACC AGC GCC GTC CTG GAG GCC
L R E A H P I V E K I L Q Y R E L T
CTC CGC GAG GCC CAC CCC ATC GTG GAG AAG ATC CTG CAG TAC CGG GAG CTC ACC
K L K S T Y I D P L P D L I H P R T
AAG CTG AAG AGC ACC TAC ATT GAC CCC TTG CCG GAC CTC ATC CAC CCC AGG ACG
G R L H T R F N Q T A T A T G G G CTA AGT
GGC CGC CTC CAC ACC CGC TTC AAC CAG ACG GCC ACG GGC AGG CTA AGT
S S D P N L Q N I P V R T P L G Q R
AGC TCC GAT CCC AAC CTC CAG AAC ATC CCC GTC CGC ACC CCG CTT GGG CAG AGG
I R R A F I A E E G W L L V A L D Y
ATC CGC CGG GCC TTC ATC GCC GAG GAG GGG TGG CTA TTG GTG GCC CTG GAC TAT
S Q I E L R V L A H L S G D E N L I
AGC CAG ATA GAG CTC AGG GTG CTG GCC CAC CTC TCC GGC GAC GAG AAC CTG ATC
R V F Q E G R D I H T E T A S W M F
CGG GTC TTC CAG GAG GGG CGG GAC ATC CAC ACG GAG ACC GCC AGC TGG ATG TTC

Replacement Figure

[illegible]

Replacement Figure

Figure 1700

Tag DNA polymerase- Sac7d fusion protein

Nucleotide sequence (SEQ ID NO: 65) //Nucleotide sequence (SEQ ID NO: 69)
Amino acid sequence (SEQ ID NO: 66) /Amino acid sequence (SEQ ID NO: 70)

```

      G   G   G
      // GGC GGC GGT

V   T   S   G   G   M   L   P   L   F   E   P   K   G   R   V   L   L   V
GTC ACT AGT GGG ATG CTG CTG CCC CTC TTT GAG CCC AAG GGC CGG GTC CTC CTG GTG

D   G   H   H   L   A   Y   R   T   F   H   A   L   K   G   L   T   T
GAC GGC CAC CAC CTG GCC TAC CGC ACC TTC CAC GCC CTG AAG GGC CTC ACC ACC

S   R   G   E   P   V   Q   A   V   Y   G   F   A   K   S   L   L   K
AGC CGG GGG GAG CCG GTG CAG GCG GTC TAC GGC TTC GCC AAG AGC CTC CTC AAG

A   L   K   E   D   G   D   A   V   I   V   V   F   D   A   K   A   P
GCC CTC AAG GAG GAC GGG GAC GCG GTG ATC GTG GTC TTT GAC GCC AAG GCC CCC

S   F   R   H   E   A   Y   G   G   Y   K   A   G   R   A   P   T   P
TCC TTC CGC CAC GAG GCC TAC GGG GGG TAC AAG GCG GGC CGG GCC CCC ACG CCA

E   D   F   P   R   Q   L   A   L   I   K   E   L   V   D   L   L   G
GAG GAC TTT CCC CGG CAA CTC GCC CTC ATC AAG GAG CTG GTG GAC CTC CTG GGG

L   A   R   L   E   V   P   G   Y   E   A   D   D   V   L   A   S   L
CTG GCG CGC CTC GAG GTC CCG GGC TAC GAG GCG GAC GAC GTC CTG GCC AGC CTG

A   K   K   A   E   K   E   G   Y   E   V   R   I   L   T   A   D   K
GCC AAG AAG GCG GAA AAG GAG GGC TAC GAG GTC CGC ATC CTC ACC GCC GAC AAA
```

D L Y Q L L L S D R I H V L H P E G Y
GAC CTT TAC CAG CTC CTT TCC GAC CGC ATC CAC GTC CTC CAC CCC GAG GGG TAC

L I T P A W L W E K Y G L R P D Q W
CTC ATC ACC CCG GCC TGG CTT TGG GAA AAG TAC GGC CTG AGG CCC GAC CAG TGG

A D Y R A L T G D E S D N L P G V K
GCC GAC TAC CGG GCC CTG ACC GGG GAC GAG TCC GAC AAC CTT CCC GGG GTC AAG

G I G E K T A R K L L E E W G S L E
GGC ATC GGG GAG AAG ACG GCG AGG AAG CTT CTG GAG GAG TGG GGG AGC CTG GAA

A L L K N L D R L K P A I R E K I L
GCC CTC CTC AAG AAC CTG GAC CGG CTG AAG CCC GCC ATC CGG GAG AAG ATC CTG

A H M D D L L K L S W D L A K V R T D
GCC CAC ATG GAC GAT CTG AAG CTC TCC TGG GAC CTG GCC AAG GTG CGC ACC GAC

L P L E V D F A K R R E P D R E R L
CTG CCC CTG GAG GTG GAC TTC GCC AAA AGG CGG GAG CCC GAC CGG GAG AGG CTT

R A F L E R L E F G S L L H E F G L
AGG GCC TTT CTG GAG AGG CTT GAG TTT GGC AGC CTC CTC CAC GAG TTC GGC CTT

L E S P K A L E E A P W P P E G A
CTG GAA AGC CCC AAG GCC CTG GAG GAG GCC CCC TGG CCC CCG GAA GGG GCC

F V G F V L S R K E P M W A D L L A
TTC GTG GGC TTT GTG CTT TCC CGC AAG GAG CCC ATG TGG GCC GAT CTT CTG GCC

L A A A R G G R V H R A P E P Y K A
CTG GCC GCC AAG GCC GGG GGC CCG GTC CAC CGG GCC CCC GAG CCT TAT AAA GCC

L R D L K E A R G L L A K D L S V L
CTC AGG GAC CTG AAG GAG GCG CCG GGG CTT CTC GCC AAA GAC CTG AGC GTT CTG

A L R E G L G L P P G D D P M L L A
GCC CTG AGG GAA GGC CTT GGC CTC CCG CCC GGC GAC GAC CCC ATG CTC CTC GCC

Replacement Figure

Y L L L D P S N T T P E G V A R R Y G
TAC CTC CTG GAC CCT TCC AAC ACC ACC CCC GAG GGG GTG GCC CGG CGC TAC GGC

G E W T E E A G E R A A L S E R L F
GGG GAG TGG ACG GAG GAG GCG GGG GAG CGG GCC GCG CTT TCC GAG AGG CTC TTC

A N L L W G R L E G E E R L L W L Y R
GCC AAC CTG TGG GGG AGG CTT GAG GGG GAG AGG CTC CTT TGG CTT TAC CGG

E V E R P L S A V L A H M E A T G V
GAG GTG GAG AGG CCC CTT TCC GCT GTC CTG GCC CAC ATG GAG GCC ACG GGG GTG

R L D V A Y L R A L S L E V A E E I
CGC CTG GAC GTG GCC TAT CTC AGG GCC TTG TCC CTG GAG GTG GCC GAG GAG ATC

A R L E A E V F R L A G H P F N L N
GCC CGC CTC GAG GCC GAG GTC TTC CGC CTG GCC CAC CCC TTC AAC CTC AAC

S R D Q L E R V L F D E L G L P A I
TCC CGG GAC CAG CTG GAA AGG GTC CTC TTT GAC GAG CTA GGG CTT CCC GCC ATC

G K T E K T G K R S T S A A V L E A
GGC AAG ACG GAG AAG ACC GGC AAG CGC TCC ACC AGC GCC GTC CTG GAG GCC

L R E A H P I V E K I L Q Y R E L T
CTC CGC GAG GCC CAC CCC ATC GTG GAG AAG ATC CTG CAG TAC CGG GAG CTC ACC

K L K S T Y I D P L P D L I H P R T
AAG CTG AAG AGC ACC TAC ATT GAC CCC TTG CCG GAC CTC ATC CAC CCC AGG ACG

G R L H T R F N Q T A T A T G R L S
GGC CGC CTC CAC ACC CGC TTC AAC CAG ACG GCC ACG GCC AGG CTA AGT

S S D P N L Q N I P V R T P L G Q R
AGC TCC GAT CCC AAC CTC CAG AAC ATC CCC GTC CGC ACC CCG CTT GGG CAG AGG

I R R A F I A E E G W L L V A L D Y

Replacement Figure

ATC CGC CGG GCC TTC ATC GCC GAG GAG GGG TGG CTA TTG GTG GCC CTG GAC TAT
 S Q I E L R V L A H L S G D E N L I
 AGC CAG ATA GAG CTC AGG GTG CTC GGC CAC CTC TCC GGC GAC GAG AAC CTG ATC
 R V F Q E G R D I H T E T A S W M F
 CGG GTC TTC CAG GAG GGG CGG GAC ATC CAC ACG GAG ACC GCC AGC TGG ATG TTC
 G V P R E A V D P L M R R A A K T I
 GGC GTC CCC CGG GAG GCC GTG GAC CCC CTG ATG CGC CGG GCC AAG ACC ATC
 N F G V L Y G M S A H R L S Q E L A
 AAC TTC GGG GTC CTC TAC GGC ATG TCG GCC CAC CGC CTC TCC CAG GAG CTA GCC
 I P Y E E A Q A F I E R Y F Q S F P
 ATC CCT TAC GAG GAG GCC CAG GCC TTC ATT GAG CGC TAC TTT CAG AGC TTC CCC
 K V R A W I E K T L E E G R R G Y
 AAG GTG CGG GCC TGG ATT GAG AAG ACC CTG GAG GAG GGC AGG AGG CGG GGG TAC
 V E T L F G R R R Y V P D L E A R V
 GTG GAG ACC CTC TTC GGC CGC CGC TAC GTG CCA GAC CTA GAG GCC CGG GTG
 K S V R E A A E R M A F N M P V Q G
 AAG AGC GTG CGG GAG GCG GCC GAG CGC ATG GCC TTC AAC ATG CCC GTC CAG GGC
 T A A D L M K L A M V K L F P R L E
 ACC GCC GCC GAC CTC ATG AAG CTG GCT ATG GTG AAG CTC TTC CCC AGG CTG GAG
 E M G A R M L L Q V H D E L V L E A
 GAA ATG GGG GCC AGG ATG CTC CTT CAG GTC CAC GAC GAG CTG GTC CTC GAG GCC
 P K E R A E A V A R L A K E V M E G
 CCA AAA GAG AGG GCG GAG GCC GTG GCC CTG GCC AAG GAG GTC ATG GAG GGG
 V Y P L A V P L E V E V G I G E D W
 GTG TAT CCC CTG GCC GTG CCC CTG GAG GTG GAG GGG ATA GGG GAG GAC TGG

Replacement Figure

L	S	A	K	E	G	I	D	G	R	G	G	G	G	H	H	H	H	H	
CTC	TCC	GCC	AAG	GAG	GAG	ATT	GAT	GGC	CGC	GGC	GGA	GGC	GGG	CAT	CAT	CAT	CAT	CAT	
H	H	//																	
CAT	CAT	//																	
M	V	K	K	V	K	F	K	Y	K	G	E	E	K	E	V	D	T	S	
ATG	GTG	AAG	GTA	AAG	TTC	AAG	TAT	AAG	GGT	GAA	GAG	AAA	GAA	GAA	GTA	GAC	ACT	TCA	
K	I	K	K	V	K	V	W	R	V	G	K	M	V	S	F	T	Y	D	
AAG	ATA	AAG	AAG	GTT	TGG	AGA	GTA	GGC	AAA	ATG	GTG	TCC	TTT	ACC	TAT	GAC	GAC		
N	G	K	T	G	R	G	A	V	S	E	K	D	A	P	K	E	L		
AAT	GGT	AAG	ACA	GGT	AGA	GGA	GCT	GTA	AGC	GAG	AAA	GAT	GCT	CCA	AAA	GAA	TTA		
L	D	M	L	A	R	A	E	R	E	K	K	//	*						
TTA	GAC	ATG	TTA	GCA	AGA	GCA	GAA	AGA	GAG	AAG	AAA	//	TAG						

Figure 17PP

Pfu DNA Polymerase (WT) -Sac7d fusion protein

Nucleotide sequence (SEQ ID NO: 61) // Nucleotide sequence (SEQ ID NO: 69)

//
ccctggtcct ggggccacat atatgttctt actgccttt atgaagaatc cccagtcgc
tctaacctgg gttatagtga caatcttcc tccaccaccg cccaagaagg ttatttctat
caactctaca cctcccctat tttctctctt atgagatttt taagtatagt tatagagaag
gttttatact ccaaaactgag ttagtagata tgtggggagc ataatgattt tagatgtgga

ttacataact gaagaaggaa aacctgttat taggctattc aaaaaagaga acgaaaaatt
taagatagag catgatagaa ctttttagacc atacatttac gctctttctca gggatgatctc
aaagattgaa gaagttaaga aaataacggg gaaaggcat ggaaagattg tgagaattgt
tgatgtagag aaggttgaga aaaagtttct cggcaagcct attaccgtgt ggaaacttta
tttggaacat cccaagatg ttcccactat tagagaaaaa gttagagAAC atccagcagt
tgtggacatc ttcgaatacg atattccatt tgcaaaagaga tacctcatcg acaaaggcct
aataccaatg gagggggaag aagagctaaa gattcttgcc ttcgatatag aaaccctcta
tcacgaagga gaagagtttg gaaaaggccc aattataatg attagttatg cagatgaaaa
tgaaagcaaa gtgattactt ggaaaaacat agatcttcca tacgttgagg ttgtatcaag
cgagagagag atgataaaga gattttctcag gattatcagg gaaaggatc ctgacattat
agttacttat aatggagact cattcgactt cccatattta gcgaaaaggg cagaaaaact
tgggattaaa ttaaccattg gaagagatgg aagcgagccc aagatgcaga gaataggcga
tatgacggct gtagaagtca agggaagaat acatttcgac ttgtatcatg taataacaag
gacaataaat ctcccaacat acacactaga ggctgtatat gaagcaattt ttggaaagcc
aaaggagaag gtatacgccg acgagatagc aaaagcctgg gaaagtggag agaaccctga
gagagttgcc aaatactcga tggaagatgc aaaggcaact tatgaactcg gaaagaatt
ccttccaatg gaaattcagc tttcaagatt agttggaca ccttatggg atgtttcaag
gtcaagcaca gggaaccttg tagagtgggt cttacttagg aaagcctacg aaagaaacga
agtagctcca aacaagccaa gtgaagagga gtatcaaga aggctcaggg agagctacac

Replacement Figure

aggtaggattc gttaaagagc cagaaaaggg gtgtgtggaa aacatagtat acctagattt
tagagcccta tatccctcga ttataattac ccacaatgtt tctcccgata ctctaaatct
tgagggatgc aagaactatg atatcgctcc tcaagtaggc cacaagtctt gcaaggacat
ccctggtttt ataccaagtc tcttgggaca ttgttagag gaaagacaaa agattaagac
aaaaatgaag gaaactcaag atcctataga aaaatactc cttgactata gacaaaaagc
gataaaactc ttagcaaatt ctttctacgg atattatggc tatgcaaaag caagatggta
ctgtaaggag tgtgctgaga gcgttactgc ctggggaaga aagtacatcg agttagtatg
gaaggagctc gaagaaaagt ttggatttaa agtcctctac attgacactg atggtctcta
tgcaactatc ccaggaggag aaagtgagga aataaagaaa aaggctctag aatttgtaaa
atacataaat tcaaagctcc ctggactgct agagcttgaa tatgaagggt ttataagag
gggattcttc gttacgaaga agaggatatgc agtaatagat gaagaaggaa aagtcattac
tcgtgggtta gagatagtta ggagagattg gagtgaattt gcaaaagaaa ctcaagctag
agtttttgag acaatactaa aacacggaga tgttgaagaa gctgtgagaa tagtaaaaga
agtaatacaa aagcttgcca attatgaaat tccaccagag aagctcgcaa tatatgagca
gataacaaga ccattacatg agtataaggc gataggctct cacgtagctg ttgcaaaagaa
actagctgct aaaggagtta aaataaagcc aggaatggta attggataca tagtacttag
aggcgatggc ccaattagca atagggaat tctagctgag gaatacgatc ccaaaaagca
caagtatgac gcagaatatt acattagaa ccaggttctt ccagcggtac ttaggatatt
ggagggattt ggatacagaa aggaagacct cagataccaa aagacaagac aagtcggcct

Replacement Figure

aacttcctgg cttaacatta aaaatccta gaaaagcgat agatatcaac ttttatctctt
tctaaccctt ttctatgaaa gaagaactga gcaggaatta ccagttcttc cgttatcttta
tgggtaatta aaaaccctatg ctcttgggag aatcttcgaa taaaatccct aacttcaggc
tttgctaagt gaatagaata aacaacatca ctcaattcaa acgccttcgt tagaaatggt
ctatctgcat gcttctcttg ctcggaannng gaggattcat aacaacagta tcaacattct
cagagaattg agaaacatca gaaactttga cttctacaac atttctaaact ttgcaactct
tcaagatttt ctaaaagaat tttaacggcc tcctcgtcaa ttctcgacgac gtagatcttt
tttgctccaa gcagagccgc tccaatggat aacacccctg ttcccgacc caagtccgct
acaatttttt ccttgtatct cctaattgtat aagcaagcca aaggagagta gatgctacct
ttccgggagt ttgtattgc tctagccaag gtttgggatt ttggaatcct ttaactctgg
aaagtataat ttcaagctcc ttcttcttca tgacagatga aaaattgttt tgtctctttt
taacttttac agaaataact gtctcaaat atgacaactc ttgacatttt tacttcatta
ccagggtaat gttttttaagt atgaaatttt tctttcatag aggaggnnnn nngtcctctc
ctcgatttcc ttggttgtgc tccatatgat aagcttccaa agtgggtgtt cagactttta
gacactcaaa taccagacga caatgggtg ctcaactcaag cccatatgg gttgagaaaa
gtagaagcgg cactactcag atgcttcccc aggaatgagg ttgtttagc tcntcccnnga
aagattgaga tgttcttgg //

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA

Replacement Figure

TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA //TGA

Figure 17QQ

Sac7d - Pfu DNA Polymerase (WT) fusion protein

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 61)

```
// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
   AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
   AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
   TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA //
//
ccctggtcct ggggccacat atatgttctt actgccttt atgaagaatc cccagtcgc
tctaacctgg gttatagtga caaatcttcc tccaccaccg cccaagaagg ttatttctat
caactctaca cctcccctat tttctctctt atgagatttt taagtatagt tatagagaag
gttttatact ccaaaactgag ttagtagata tgtggggagc ataatgattt tagatgtgga
ttacataact gaagaaggaa aacctgttat taggctattc aaaaaagaga acggaaaatt
taagatagag catgatagaa ctttttagacc atacatttac gctcttctca gggatgattc
aaagattgaa gaagttaaga aaataacggg ggaaaggcat ggaaagattg tgagaattgt
tgatgtagag aagggtgaga aaaagtctt cggcaagcct attaccgtgt ggaaacttta
tttggaacat cccaagatg ttcccactat tagagaaaaa gtagagaaac atccagcagt
tgtggacatc ttcgaatacg atattccatt tgcaaaagaga tacctcatcg acaaaggcct
aataccaatg gagggggaag aagagctaaa gattcttgcc ttcgatatag aaaccctcta
```

Replacement Figure

tcacgaagga gaagagtttg gaaaaggccc aattataatg attagttatg cagatgaaaa
tgaaagcaag gtgattactt ggaaaaacat agatcttcca tacgttgagg ttgtatcaag
cgagagagag atgataaaga gatttctcag gattatcagg gagaaggatc ctgacattat
agttacttat aatggagact cattcgactt cccatattta gcgaaaaagg cagaaaaact
tgggattaaa ttaaccattg gaagagatgg aagcgagccc aagatgcaga gaataggcga
tatgacggct gtagaagtca agggaagaat acatttcgac ttgtatcatg taataacaag
gacaataaat ctccaacat acacactaga ggctgtatat gaagcaattt ttggaaaagcc
aaaggagaag gtatacgccg acgagatagc aaaagcctgg gaaagtggag agaaccctga
gagagtggcc aaatactcga tggaagatgc aaaggcaact tatgaactcg ggaaagaatt
ccttccaatg gaaattcagc tttcaagatt agttggacaa cctttatggg atgtttcaag
gtcaagcaca gggaaacctg tagagtggtt ctacttagg aaagcctacg aaagaaaacga
agtagctcca acaagccaa gtgaagagga gtatcaaga aggctcaggg agagctacac
agggtggattc gttaaagagc cagaaaaagg gtgtgtggaa aacatagtat acctagattt
tagagcccta tatccctcga ttataattac ccacaatgtt tctcccgata ctctaaatct
tgagggatgc aagaactatg atatcgctcc tcaagtaggc cacaagtctt gcaaggacat
ccctgggttt ataccaagtc tcttgggaca tttgttagag gaaagacaaa agattaagac
aaaaatgaag gaaactcaag atcctataga aaaatactc cttgactata gacaaaaagc
gataaaactc ttagcaaatt ctttctacgg atattatggc tatgcaaaag caagatggta
ctgtaaggag tgtgctgaga gcgttactgc ctggggaaga aagtacatcg agttagtatg

Replacement Figure

gaaggagctc gaagaaaagt ttggatttaa agtcctcttac attgacactg atgggtctcta
tgcaactatc ccaggaggag aaagtgagga aataaagaaa aaggctctag aatttgtaaa
atacataaat tcaaagctcc ctggactgct agagcttgaa tatgaagggt ttataagag
gggattcttc gttacgaaga agaggtatgc agtaatagat gaagaaggaa aagtcattac
tcgtgggtta gagatagtta ggagagattg gagtgaatt gcaaaagaaa ctcaagctag
agttttggag acaatactaa aacacggaga tgttgaagaa gctgtgagaa tagtaaaaga
agtaatacaa aagcttgcca attatgaaat tccaccagag aagctcgcaa tatatgagca
gataacaaga ccattacatg agtataaggc gataggtcct cacgtagctg ttgcaaaagaa
actagctgct aaaggagtta aaataaagcc aggaatggtta attggataca tagtacttag
aggcgatggt ccaattagca atagggcaat tctagctgag gaatacgatc ccaaaaagca
caagtatgac gcagaatatt acattgagaa ccaggttctt ccagcggtag ttaggatatt
ggagggattt ggatacagaa aggaagacct cagataccaa aagacaagac aagtcggcct
aacttcctgg cttaacatta aaaaatccta gaaaagcgat agatatcaac ttttatctt
tctaaccttt ttctatgaaa gaagaactga gcaggaatta ccagttcttc cgttatttta
tgggtaatta aaaaccatg ctcttgggag aatcttcgaa taaaatccct aacttcaggc
tttgctaagt gaatagaata aacaacatca ctacttcaa acgccttcgt tagaaatggt
ctatctgcat gcttctcttg ctcggaanng gaggattcat aacaacagta tcaacattct
cagagaattg agaaacatca gaaactttga ctctacaac atttctaact ttgcaactct
tcaagatttt ctaaaagaat ttaacggcc tcctcgtcaa ttctgacgac gtagatcttt

Replacement Figure

tttgctcaa gcagagccgc tccaatggat aacacccctg ttcccgacc caagtccgct
acaattttt ccttgtatct cctaattgat aagcaagcca aaggagagta gatgctacct
ttccgggagt tttgtattgc ttagccaag gtttgggatt tttgaatcct ttaactctgg
aaagtataat ttcaagctcc ttcttcttca tgacagatga aaaattgttt tgtctctttt
taacttttac agaaaataact gtctcaaatt atgacaactc ttgacatttt tacttcatta
ccagggtaat gttttttaagt atgaaaathtt tctttcatag aggaggnnnn nngtcctctc
ctcgatttcc ttggttgtgc tccatatgat aagcttccaa agtgggtgtt cagactttta
gacactcaaa taccagacga caatgggtgtg ctactcaag ccccatatgg gttgagaaaa
gtagaagcgg cactactcag atgcttcccc aggaatgagg ttgtttagc tcntccnga
aagattgaga tgttcttgg // TGA

Figure 17RR

Sac7d - PFU DNA POLYMERASE (V93 R OR E) fusion protein

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 27)

Nucleotide sequence (SEQ ID NO: 69) //Nucleotide sequence (SEQ ID NO: 28)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA //

ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTGAAGAAA AGTTTCTCGG CAAGCCTATT 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAAGAAA CAAGATXXXC CCACATATTAG AGAAAAAGTT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATXXXC CCACATATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCCTC 420
GATATAGAAA CCCTCTATCA CGAAGGAGAA GAGTTTGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAAATGA AGCAAAGGTG ATTACTTTGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCC ATATTTAGCG 660
AAAAGGCGAG AAAA ACTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTTCGACTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTGG GAAAGCCAAA GGAGAAAGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
GAACTCGGGA AAGAAATCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTC AAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140
CTCAGGGAGA GCTACACAGG TGGATTCCGT AAAGAGCCAG AAAAGGGGT GTGGGAAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAAAGCGAT AAAACTCTTA GCAAAATCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCCTG GGGAAAGAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAATTTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAAG 1980

Replacement Figure

CTCGCAATAT ATGAGCAGAT AACAAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCCTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAA TAAAGCCAGG AATGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTCTTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280
ACAAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAA AATCC //
// TGA 2328

Figure 17SS

PFU DNA POLYMERASE (V93 R OR E) -Sac7d fusion protein

Nucleotide sequence (SEQ ID NO: 27) // Nucleotide sequence (SEQ ID NO: 69)
Nucleotide sequence (SEQ ID NO: 28) // Nucleotide sequence (SEQ ID NO: 69)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTACGCT 120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAA TAACGGGGGA AAGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATXXXC CCACTATTAG AGAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCCTC 420
GATATAGAAA CCCTCTATCA CGAAGGAGAA GAGTTTGGA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGA AAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCT ATATTTAGCG 660
AAAAGGGCAG AAAAACTTGG GATTAAATTA ACCATTGGA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTGG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
GAACTCGGGA AAGAAATTCCT TCCAATGGAA ATTACGCTTT CAAGATTAGT TGGACAACTT 1020

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TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAGAAGG 1140
CTCAGGGAGA GCTACACAGG TGGATTTCGT AAAGAGCCAG AAAAGGGGT GTGGGAAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCCT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTA CTGCTG GGAAGAAAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAAATTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCCTCAC 2040
GTAGCTGTTG CAAAGAACT AGCTGCTAAA GGAGTTAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCCTTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTGGA TACAGAAAAG AAGACCTCAG ATACCAAAAAG 2280
ACAAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC // 2328

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
   AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
   AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
   TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA // TGA

```

Figure 17TT

PFU DNA POLYMERASE (G387P/V93R OR E) -Sac7d fusion protein

Nucleotide sequence (SEQ ID NO: 29) // Nucleotide sequence (SEQ ID NO: 69)
Nucleotide sequence (SEQ ID NO: 30) // Nucleotide sequence (SEQ ID NO: 69)

G387P Mutant (CCN is the codon for Proline where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAA 60
AAAGAGAACG GAAAATTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTACGCT 120
CTTCTCAGGG ATGATTCAA GATTGAAGAA GTTAAGAAA TAACGGGGA AAGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAA GTTTCTCGG AGTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATT GGAACATCCC CAAGATXXXC CCACTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCCTC 420
GATATAGAAA CCCTCTATCA CGAAGGAGAA GAGTTTGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAAATGA AGCAAAGGTG ATTACTTTGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCT ATATTAGCG 660
AAAAGGGCAG AAAAAGCTGG GATTAAATTA ACCATTGGA AGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGA 840
GCAATTTTGG GAAAGCCAAA GGAGAAAGTA TACGCCGACG AGATAGCAAA AGCCTGGGA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
GAACTCGGGA AAGAAATCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAGGTC AAGCACAGGG AACCTTGTA AGTGGTTCTT ACTTAGGAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAAG 1140
CTCAGGGAGA GCTACACACC NGGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGTACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCCTGA AGGACATCCC TGGTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAAATCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGTAATG GAGGAGTGT TAAGGAGTGT GCTGAGAGCG TTACTGCCCTG GGAAGAAAAG 1560
TACATCGAGT TAGTATGGA GGAGCTCGAA GAAAAGTTTG GATTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAG 1680
GCTCTAGAA TTTGTAATAA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAATTTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAAGACCA TTACATGAGT ATAAGGCGAT AGGTCTCTAC 2040

Replacement Figure

GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
 GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
 TACGATCCCA AAAAGCACAA GTATGACGCA GAAATATTACA TGGAGAACCA GGTTCCTCCA 2220
 GCGGTACTTA GGATATTGGA GGGATTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280
 ACAAGACAAG TCGGCCTAAC TTCTTGCTT AACATTAAAA AATCC // 2328

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
 AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
 AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
 TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA // TGA

Figure 17UU

PFU DNA POLYMERASE (G387P/V93R OR E) -Sac7d fusion protein

Nucleotide sequence (SEQ ID NO: 29) // Nucleotide sequence (SEQ ID NO: 69)

Nucleotide sequence (SEQ ID NO: 30) // Nucleotide sequence (SEQ ID NO: 69)

G387P Mutant (CCN is the codon for Proline where N = C, G, A, or T)
 V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
 V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
 ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAC CTGTTATTAG GCTATTCAA 60
 AAAGAGAACG GAAATTTAA GATAGAGCAT GATAGAAGCTT TTAGACCATA CATTACGCT 120
 CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
 AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
 ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATXXXC CCACTATTAG AGAAAAAGTT 300
 AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTCG AAAGAGATAC 360
 CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCCTTC 420

Replacement Figure

GATATAGAAA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAAATGA AGCAAAAGGTG ATTACTTTGGA AAAACATAGA TCITTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTTCC ATATTAGCG 660
AAAAGGGCAG AAAAACTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTGG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
GAACTCGGGA AAGAAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAGGTC AAGCACAGG AACCTTGTA AGTGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140
CTCAGGGAGA GCTACACAGTTGGATTTCGTT AAAGGCCAG AAAAGGGTT GTGGAAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGACACATTT GTTAGAGGAA 1380
AGACAAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAAAGCGAT AAAACTCTTA GCAAATCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTTACTGCCCTG GGAAGAAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAATTTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAAGAGT AATACAAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAAGACCA TTACATGAGT ATAAGGCGAT AGTCCTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTCTTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC // 2328

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
TTA GAC ATG TTA GCA AGA GCA GAA AAG AAA // TGA

Replacement Figure

Figure 17VV

SAC7D-PFU DNA POLYMERASE(D141A/E143A/V93R OR E) fusion protein

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 31)

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 32)

D141A/E143A Mutant (GCN is the codon for alanine where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
TTA GAC ATG TTA GCA AGA GCA GAG AAG AAA //

//ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAC CTGTTATTAG GCTATTCAA 60
AAAGAGAACG GAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTACGCT 120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATXXXC CCACTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTGTC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAA AGCTAAAGAT TCTTGCCCTTC 420
GCNATAGCNA CCCTCTATCA CGAAGGAGAA GAGTTTGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAATGA AGCAAAAGTG ATTACTTGG AACAATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCTC ATATTAGCG 660
AAAAGGGCAG AAAAAGTTGG GATTAAATTA ACCATTGGA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTG GAAAGCCAAA GGAGAAAGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
GAACTCGGGA AAGAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACTT 1020
TTATGGGATG TTTCAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140

CTCAGGGAGA GCTACACAGTTGGATTTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTC TGCA AGGACATCCC TGGTTTATA CCAAGTCTCT TGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCCTG GGGAAAGAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGA AATTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAC ACGGAGATGT TGAAGAAAGCT 1920
GTGAGAAATAG TAAAAGAAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAAGACCA TTACATGAGT ATAAGGCGAT AGTCCTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTC TTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC // 2328

TGA

Figure 17WW

KOD DNA POLYMERASE - Sac7d fusion protein

Nucleotide sequence (SEQ ID NO: 33) // Nucleotide sequence (SEQ ID NO: 69)
Nucleotide sequence (SEQ ID NO: 34) // Nucleotide sequence (SEQ ID NO: 69)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
ATGATCCTCG ACAC TGACTA CATAACCGAG GATGGAAAGC CTGTCATAAG AATTTC AAG 60
AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT TTGAACCCCTA CTTCTACGCC 120
CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAAGA TAACCGCCGA GAGGCACGGG 180
ACGGTTGTAA CGGTTAAGCG GGTGAAAAG GTTCAGAAGA AGTCCCTCGG GAGACCAAGT 240
GAGGTCTGGA AACTCTACTT TACTCATCCG CAGGACXXXC CAGCGATAAG GGACAAGATA 300

CGAGAGCATC CAGCAGTTAT TGACATCTAC GAGTACGACA TACCCTTCGC CAAGCGGTAC 360
CTCATAGACA AGGGATTAGT GCCAATGGAA GCGACGAGG AGCTGAAAAT GCTCGCCTTC 420
GACATTGAAA CTCCTACCA TGAGGCGAG GAGTTGCCG AGGGCCAAAT CCTATGATA 480
AGCTACGCCG ACGAGGAAGG GGCCAGGGTG ATAACTTGA AGAACGTGA TCTCCCCTAC 540
GTTGACGTCG TCTCGACGGA GAGGGAGATG ATAAAGCGCT TCCTCCGTGT TGTGAAGGAG 600
AAAGACCCGG ACGTTCTCAT AACCTACAAC GCGACAACCT TCGACTTCGC CTATCTGAAA 660
AAGCGCTGTG AAAAGCTCGG AATAAACTTC GCCCTCGAA GGGATGGAAG CGAGCCGAAG 720
ATTCAGAGGA TGGGCGACAG GTTTGCCGTC GAAGTGAAG GACGGATACA CTTCGATCTC 780
TATCCTGTGA TAAGACGGAC GATAAACCTG CCCACATACA CGCTTGAGGC CGTTTATGAA 840
GCCGTCTTCG GTCAGCCGAA GGAGAAGGTT TACGCTGAGG AAATAACCAC AGCCTGGGAA 900
ACCGCGAGA ACCTTGAGAG AGTCGCCCGC TACTCGATGG AAGATGCGAA GGTACATAC 960
GAGCTTGGA AGGAGTTCCT TCCGATGGAG GCCCAGCTTT CTCGCTTAAT CGGCCAGTCC 1020
CTCTGGGACG TCTCCCGCTC CAGCACTGGC AACCTCGTG AGTGTTCTT CCTCAGGAAG 1080
GCCTATGAGA GGAATGAGCT GGCCCCGAAC AAGCCCAGTG AAAAGGAGCT GGCCAGAAGA 1140
CGGCAGAGCT ATGAAGGAGG CTATGTAAA GAGCCCAGA GAGGGTTGTG GGAGAACATA 1200
GTGTACCTAG ATTTTAGATC CCTGTACCC CTAATCATCA TCACCCACAA CGTCTGCCG 1260
GATACGCTCA ACAGAGAAGG ATGCAAGGAA TATGACGTTG CCCACAGGT CGGCCACCGC 1320
TTCTGCAAGG ACTTCCAGG ATTTATCCG AGCCTGCTTG GAGACCTCCT AGAGGAGAGG 1380
CAGAAGATAA AGAAGAAGAT GAAGGCCACG ATTGACCCGA TCGAGAGGAA GCTCCTCGAT 1440
TACAGGCAGA GGGCCATCAA GATCCTGGCA AACAGCTACT ACGTTACTA CGGCTATGCA 1500
AGGGCGCGCT GGTA CTGCAA GGAGTGTGCA GAGAGCGTAA CGGCCTGGG AAGGAGTAC 1560
ATAACGATGA CCATCAAGGA GATAGAGGAA AAGTACGGCT TTAAGGTAAT CTACAGCGAC 1620
ACCGACGGAT TTTTGGCCAC AATACCTGGA GCCGATGCTG AAACCGTCAA AAAGAAGGCT 1680
ATGGAGTTCC TCAAGTATAT CAACGCCAAA CTTCGGGCG CGCTTGAGCT CGAGTACGAG 1740
GGCTTCTACA AACGCGGCTT CTTCGTCACG AAGAAGAAGT ATGCGGTGAT AGACGAGGAA 1800
GGCAAGATAA CAACGCGCGG ACTTGAGATT GTGAGGCGTG ACTGGAGCGA GATAGCGAAA 1860
GAGACGCAGG CGAGGGTTCT TGAAGCTTG CTAAAGGACG GTGACGTCGA GAAGGCCGTG 1920
AGGATAGTCA AAGAAGTTAC CGAAAAGCTG AGCAAGTACG AGGTTCCGCC GGAGAAGCTG 1980
GTGATCCACG AGCAGATAAC GAGGGATTTA AAGGACTACA AGGCAACCGG TCCCCACGTT 2040
GCCGTTGCCA AGAGGTTGGC CGCGAGAGGA GTCAAAATAC GCCCTGGAAC GGTGATAAGC 2100
TACATCGTGC TCAAGGGCTC TGGGAGGATA GCGACAGGG CGATACCGTT CGACGAGTTC 2160
GACCCGACGA AGCACAAGTA CGACGCCGAG TACTACATTG AGAACCAAGT TCTCCAGCC 2220
GTTGAGAGAA TTCTGAGAGC CTTGCGTTAC CGCAAGGAAG ACCTGCGCTA CCAGAAGACG 2280
AGACAGGTTG GTTTGAGTGC TTGGCTGAAG CCGAAGGGA CT 2325
// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA // TGA

Replacement Figure

Figure 17XX

Sac7d - KOD DNA POLYMERASE fusion protein

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 33)

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 34)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA //

//ATGATCCTCG ACACTGACTA CATAACCGAG GATGAAAGC CTGTCATAAG AATTTCAAG 60
AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACGGACTT TTGAACCCTA CTTCTACGCC 120
CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAAGA TAACCGCCGA GAGGCACGG 180
ACGGTTGTAA CGGTTAAGCG GGTGAAAAG GTTCAGAAGA AGTTCCCTCG GAGACCAGTT 240
GAGGTCTGGA AACTCTACTT TACTCATCCG CAGGACXXXC CAGCGATAAG GGACAAGATA 300
CGAGAGCATC CAGCAGTTAT TGACATCTAC GAGTACGACA TACCCTTCGC CAAGCGCTAC 360
CTCATAGACA AGGGATTAGT GCCAATGGAA GCGACGAGG AGCTGAAAAT GCTCGCCTTC 420
GACATTGAAA CTCTCTACCA TGAGGCGGAG GAGTTCGCC AGGGCCCAAT CCTTATGATA 480
AGCTACGCCG ACGAGGAAGG GGCCAGGGTG ATAACTTGA AGAACGTGGA TCTCCCTAC 540
GTTGACGTCG TCTCGACGGA GAGGGAGATG ATAAAGCGCT TCCTCCGTGT TGTGAAGGAG 600
AAAGACCCCG ACGTTCTCAT AACCTACAAC GCGACAACCT TCGACTTCGC CTATCTGAAA 660
AAGCGCTGTG AAAAGCTCGG AATAAACTTC GCCCTCGGAA GGGATGGAAG CGAGCCGAAG 720
ATTCAGAGGA TGGGCGACAG GTTTGCCGTC GAAGTGAAGG GACGGATACA CTTCGATCTC 780
TATCCTGTGA TAAGACGGAC GATAAACCTG CCCACATACA CGCTTGAGGC CGTTTATGAA 840
GCCGTCTTCG GTCAGCCGAA GGAGAAGGTT TACGCTGAGG AAATAACCCAC AGCCTGGGAA 900
ACCGGCGAGA ACCTTGAGAG AGTCGCCCGC TACTCGATGG AAGATGCGAA GGTACATAC 960
GAGCTTGGGA AGGAGTTCCT TCCGATGGAG GCCCAGCTTT CTCGCTTAAT CGGCCAGTCC 1020
CTCTGGGACG TCTCCCGCTC CAGCACTGGC AACCTCGTTG AGTGGTTCCT CCTCAGGAAG 1080
GCCTATGAGA GGAATGAGCT GGCCCCGAAC AAGCCCGATG AAAAGGAGCT GGCCAGAAGA 1140
CGGCAGAGCT ATGAAGGAGG CTATGTAAAA GAGCCCGAGA GAGGTTGTG GGAGAACATA 1200
GTGTACCTAG ATTTTAGATC CCTGTACCCC TCAATCATCA TCACCCACAA CGTCTCGCCG 1260

GATACGCTCA ACAGAGAAGG ATGCAAGGAA TATGACGTTG CCCACAGGT CGGCCACCGC 1320
TTCTGCAAGG ACTTCCCAGG ATTTATCCCG AGCCTGCTTG GAGACCTCCT AGAGGAGAGG 1380
CAGAAGATAA AGAAGAAGAT GAAGGCCACG ATTGACCCGA TCGAGAGGAA GCTCCTCGAT 1440
TACAGGCAGA GGGCCATCAA GATCCTGGCA AACAGCTACT ACGTTACTA CGGCTATGCA 1500
AGGGCGCGCT GGTA CTGCAA GGAGTGTGCA GAGAGCGTAA CGGCCTGGG AAGGAGTAC 1560
ATAACGATGA CCATCAAGGA GATAGAGGAA AAGTACGGCT TTAAGGTAAT CTACAGCGAC 1620
ACCGACGGAT TTTTGGCCAC AATACCTGGA GCCGATGCTG AAACCGTCAA AAAGAAGGCT 1680
ATGGAGTTCC TCAAGTATAT CAACGCCAAA CTTCCGGGCG CGCTTGAGCT CGAGTACGAG 1740
GGCTTCTACA AACCGGCTT CTTCGTCACG AAGAAGAAGT ATGCGGTGAT AGACGAGGAA 1800
GGCAAGATAA CAACGCGCGG ACTTGAGATT GTGAGGCGTG ACTGGAGCGA GATAGCGAAA 1860
GAGACGCAGG CGAGGGTTCT TGAAGCTTTG CTAAAGGACG GTGACGTCGA GAAAGCCGTG 1920
AGGATAGTCA AAGAA GTTAC CGAAAAGCTG AGCAAGTACG AGGTTCCGCC GGAGAAAGCTG 1980
GTGATCCACG AGCAGATAAC GAGGGATTTA AAGGACTACA AGGCAACCCG TCCCCACGTT 2040
GCCGTTGCCA AGAGGTTGGC CGCGAGAGGA GTCAAAATAC GCCCTGGAAC GGTGATAAGC 2100
TACATCGTGC TCAAGGGCTC TGGGAGGATA GCGCACAGG CGATACCGTT CGACGAGTTC 2160
GACCCGACGA AGCACAAGTA CGACGCCGAG TACTACATTG AGAACCAAGT TCTCCAGCC 2220
GTTGAGAGAA TTCTGAGAGC CTTCCGGTTAC CGCAAGGAAG ACCTGCGCTA CCAGAAAGACG 2280
AGACAGGTTG GTTTGAGTGC TTGGCTGAAG CCGAAGGGAA CT //TAG 2325

Figure 17YY

Sac7d-Vent DNA POLYMERASE FUSION PROTEIN

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 35)
Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 36)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAA //

ATGATACTGG ACACTGATTA CATAACAAAA GATGGCAAGC CTATAATCCG AATTTTAAG 60
AAAGAGAACG GGGAGTTTAA AATAGAAGTT GACCTCATTTTCAGCCCTA TATATATGCT 120
CTTCTCAAAG ATGACTCCGC TATTGAGGAG ATAAAGGCAA TAAAGGGCGA GAGACATGGA 180

Replacement Figure

AAAAAGTGTGA GAGTGCTCGA TGCAGTGAAA GTCAGGAAAA AATTTTGGG AAGGGAAGTT 240
 GAAGTCTGGA AGCTCATTTT CGAGCATCCC CAAGACXXXC CAGCTATGCG GGGCAAAATA 300
 AGGGAACATC CAGCTGTGGT TGACATTTAC GAATATGACA TACCTTTTGC CAAGCGTTAT 360
 CTCATAGACA AGGGCTTGAT TCCCATGGAG GGAGACGAGG AGCTTAAGCT CCTTGCCTTT 420
 GATATTGAAA CGTTTATCA TGAGGGAGAT GAAATTGGAA AGGCGAGAT AATAATGATT 480
 AGTTATGCCG ATGAAGAAGA GGCCAGAGTA ATCACATGGA AAAATATCGA TTTGCCGTAT 540
 GTCGATGTTG TGTCCAATGA AAGAGAAATG ATAAAGCGTT TTGTTCAAGT TGTAAAGAA 600
 AAAGACCCCG ATGTGATAAT AACTTACAAT GGGACAATT TTGATTTGCC GTATCTCATA 660
 AAACGGGCAG AAAAGCTGGG AGTTCGGCTT GTCTTAGGAA GGGACAAAGA ACATCCCGAA 720
 CCCAAGATTC AGAGGATGGG TGATAGTTTT GCTGTGAAA TCAAGGGTAG AATCCACTTT 780
 GATCTTTTCC CAGTTGTGCG AAGGACGATA AACCTCCCAA CGTATACGCT TGAGGCAGTT 840
 TATGAAGCAG TTTTAGGAAA AAGAAAGCAT GAAAAAATA GCCAGTACT CAATGGAAGA TGCTAGGCA 900
 TGGGAAACAG AAGAAAGCAT GAAAAAATA GCCAGTACT CAATGGAAGA TGCTAGGCA 960
 ACGTATGAGC TCGGGAAGGA ATTCTTCCCG ATGGAAGCTG AGCTGGCAAA GCTGATAGGT 1020
 CAAAGTGAT GGGACGTC CAGATCAAGC ACCGGCAACC TCGTGGAGTG GTATCTTTA 1080
 AGGGTGGCAT ACGCGAGGAA TGAACCTTGCA CCGAACAAAC CTGATGAGGA AGAGTATAA 1140
 CGGCGCTTAA GAACAACCTTA CCTGGGAGGA TATGTAAAAG AGCCAGAAAA AGGTTTGTGG 1200
 GAAAATATCA TTTATTTTGA TTTCCGCAGT CTGTACCCCTT CAATAATAGT TACTCACAA 1260
 GTATCCCCAG ATACCCCTTGA AAAAGAGGGC TGTAAAGATT ACGATGTTGC TCCGATAGTA 1320
 GGATATAGGT TCTGCAAGGA CTTTCCGGGC TTTATTCCTT CCATACCTCG GACTTAAAT 1380
 GCAATGAGGC AAGATATAA GAAGAAAATG GAATCCACAA TTGACCCGAT CGAAAAAGAA 1440
 ATGCTCGATT ATAGGCAAAG GGCTATTAAA TTGCTTGCAA ACAGCTATTA CGGCTATATG 1500
 GGGTATCCTA AGGCAAGATG GTACTCGAAG GAATGTGCTG AAAGCGTTAC CGCATGGGG 1560
 AGACACTACA TAGAGATGAC GATAAGAGAA ATAGAGGAAA AGTTCGGCTT TAAGGTTCTT 1620
 TATGCGGACA CTGACGGCTT TTATGCCACA ATACCCGGGG AAAAGCCTGA ACTCATTA 1680
 AAGAAAGCCA AGGAATTCCT AAACCTACATA AACTCCAAAC TTCCAGGTCT GCTTGAGCTT 1740
 GAGTATGAGG GCTTTTACTT GAGAGGATTC TTTGTTACAA AAAAGCGCTA TGCAGTCATA 1800
 GATGAAGAGG GCAGGATAAC AACAAAGGGC TTGGAAGTAG TAAAGGAGAG TTGGAGTGAG 1860
 ATAGCTAAGG AGACTCAGGC AAAGGTTTGA GAGGCTATAC TTAAGAGAGG AAGTGTGAA 1920
 AAAGCTGTAG AAGTTGTTAG AGATGTTGTA GAGAAAATAG CAAAATACAG GGTTCCTT 1980
 GAAAAGCTTG TTATCCATGA GCAGATTACC AGGGATTAA AGGACTACAA AGCCATTGGC 2040
 CCTCATGTG CGATAGCAA AAGACTTGCC GCAAGAGGGA TAAAAGTGAA ACCGGGACA 2100
 ATAATAAGCT ATATCGTTCT CAAAGGGAGC GGAAGATAA GCGATAGGGT AATTTTACTT 2160
 ACAGAATACG ATCCTAGAAA ACACAAGTAC GATCCGGACT ACTACATAGA AAACCAAGTT 2220
 TTGCCGGCAG TACTTAGGAT ACTCGAAGCG TTTGGATACA GAAAGGAGGA TTTAAGGTAT 2280
 CAAAGCTCAA AACAAACCGG CTTAGATGCA TGGCTCAAGA GGTAG 2325

Replacement Figure

Figure 17ZZ

Vent DNA POLYMERASE - Sac7d FUSION PROTEIN

Nucleotide sequence (SEQ ID NO: 35) // Nucleotide sequence (SEQ ID NO: 69)

Nucleotide sequence (SEQ ID NO: 36) // Nucleotide sequence (SEQ ID NO: 69)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATACTGG ACACTGATTA CATAACAAA GATGGCAAGC CTATAATCCG AATTTTAAAG 60
AAAGAGAACG GGGAGTTTAA AATAGAACTT GACCCCTATT TTCAGCCCTA TATATATGCT 120
CTTCTCAAAG ATGACTCCGC TATTGAGGAG ATAAAGGCAA TAAAGGGCGA GAGACATGGA 180
AAAACGTGTA GAGTGCTCGA TGCAGTGAAA GTCAGGAAAA AATTTTGGG AAGGGAAGTT 240
GAAGTCTGGA AGCTCATTTT CGAGCATCCC CAAGACXXXC CAGCTATGCG GGGCAAAATA 300
AGGGAACATC CAGCTGTGGT TGACATTTAC GAATATGACA TACCCTTTGC CAAGCGTTAT 360
CTCATAGACA AGGGCTTGAT TCCCATGGAG GGAGACGAGG AGCTTAAGCT CCTTGCCCTT 420
GATATTGAAA CGTTTATCA TGAGGGAGAT GAATTTGAA AGGGCGAGAT AATAATGATT 480
AGTTATGCCG ATGAAGAAGA GGCCAGAGTA ATCACATGGA AAAATATCGA TTTGCCGTAT 540
GTCGATGTTG TGTCCAATGA AAGAGAAATG ATAAAGCGTT TTGTTCAAGT TGTTAAAGAA 600
AAAGACCCCG ATGTGATAAT AACTTACAAT GGGACAAAT TTGATTGCG GTATCTCATA 660
AAACGGGCAG AAAAGCTGGG AGTTCGGCTT GTCTTAGGAA GGGACAAAGA ACATCCCGAA 720
CCCAAGATTC AGAGGATGGG TGATAGTTT TGATAGTAAA TCAAGGGTAG AATCCACTTT 780
GATCTTTTCC CAGTTGTGCG AAGGACGATA AACCTCCCAA CGTATACGCT TGAGGCAGTT 840
TATGAAGCAG TTTTAGGAAA AACCAAAAGC AAATTAGGAG CAGAGGAAAT TGCCGCTATA 900
TGGGAAACAG AAGAAAGCAT GAAAAAATA GCCCAGTACT CAATGGAAGA TGCTAGGGCA 960
ACGTATGAGC TCGGGAAGGA ATTCTTCCCC ATGGAAGCTG AGCTGGCAA GCTGATAGGT 1020
CAAAGTGTAT GGGACGTCTC GAGATCAAGC ACCGGCAACC TCGTGGAGTG GTATCTTTTA 1080
AGGGTGGCAT ACGCGAGGAA TGAAC TTGCA CCGAACAAC CTGATAGGA AGAGTATAAA 1140
CGGCGCTTAA GAACAACCTTA CCTGGGAGGA TATGTAAAAG AGCCAGAAAA AGGTTTGTGG 1200
GAAAATATCA TTTATTTGGA TTTCCGCAGT CTGTACCCCT CAATAATAGT TACTCACAA 1260
GTATCCCCAG ATACCCTTGA AAAAGAGGGC TGTAAGAAAT ACGATGTTGC TCCGATAGTA 1320
GGATATAGGT TCTGCAAGGA CTTTCCGGGC TTTATTCCT CCATACTCGG GGACTTAATT 1380

GCAATGAGGC AAGATATATAA GAAGAAAATG AAATCCACAA TTGACCCGAT CGAAAAAGAAA 1440
ATGCTCGATT ATAGGCAAG GGCTATTAAA TTGCTTGCAA ACAGCTATTA CGGCTATATG 1500
GGGTATCCTA AGGCAAGATG GTACTCGAAG GAATGTGCTG AAAGCGTTAC CGCATGGGG 1560
AGACACTACA TAGAGATGAC GATAAGAGAA ATAGAGGAAA AGTTCGGCTT TAAGGTTCTT 1620
TATGCGGACA CTGACGGCTT TTATGCCACA ATACCCGGG AAAAGCCTGA ACTCATTA 1680
AAGAAAGCCA AGGAATTCCT AACTACATA AACTCCAAC TTCCAGGTCT GCTTGAGCTT 1740
GAGTATGAGG GCTTTTACTT GAGAGGATTC TTTGTTACAA AAAAGCGCTA TGCAGTCATA 1800
GATGAAGAGG GCAGGATAAC AACAAAGGGC TTGGAAGTAG TAAGGAGAGA TTGGAGTGAG 1860
ATAGCTAAGG AGACTCAGG AAAGGTTTAA GAGGCTATAC TTAAGAGGG AAGTGTTGAA 1920
AAAGCTGTAG AAGTTGTTAG AGATGTTGTA GAGAAAATAG CAAAATACAG GGTTCACCTT 1980
GAAAAGCTTG TTATCCATGA GCAGATTACC AGGGAATTAA AGGACTACAA AGCCATTGGC 2040
CCTCATGTG CGATAGCAAA AAGACTTGCC GCAAGAGGA TAAAAGTGAA ACCGGGCACA 2100
ATAATAAGCT ATATCGTTCT CAAAGGGAGC GGAAGAGATA GCGATAGGT AATTTTACTT 2160
ACAGAAATACG ATCCTAGAAA ACACAAGTAC GATCCGGACT ACTACATAGA AAACCAAGTT 2220
TTGCCGGCAG TACTTAGGAT ACTCGAAGCG TTTGGATACA GAAAGGAGGA TTTAAGGTAT 2280
CAAAGCTCAA AACAAACCGG CTTAGATGCA TGGCTCAAGA GG 2325 //

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAA // TGA

Figure 17AAA

Deep Vent- Sac7d DNA polymerase fusion protein

Nucleotide sequence (SEQ ID NO: 37) // Nucleotide sequence (SEQ ID NO: 69)
Nucleotide sequence (SEQ ID NO: 38) // Nucleotide sequence (SEQ ID NO: 69)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)

V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATACTTG	ACGCTGACTA	CATCACCGAG	GATGGGAAGC	CGATATAAG	GATTTCAAG	60
AAAGAAAACG	GGAGTTTAA	GGTTGAGTAC	GACAGAAACT	TTAGACCTTA	CATTTACGCT	120
CTCCTCAAAG	ATGACTCGCA	GATTGATGAG	GTTAGGAAGA	TAACCGCCGA	GAGGCATGGG	180
AAGATAGTGA	GAATTATAGA	TGCCGAAAAG	GTAAGGAAGA	AGTTCTCTGG	GAGGCCGATT	240
GAGGTATGGA	GGCTGTACTT	TGAACACCCCT	CAGGACXXXC	CCGCAATAAG	GGATAAGATA	300
AGAGAGCATT	CCGCAGTTAT	TGACATCTTT	GAGTACGACA	TTCCGTTTCG	GAAGAGGTAC	360
CTAATAGACA	AAGGCCTAAT	TCCAATGGAA	GGCGATGAAG	AGCTCAAAGT	GCTCGCATTT	420
GACATAGAAA	CCCTCTATCA	CGAAGGGGAG	GAGTTCGCGA	AGGGGCCCAT	TATAATGATA	480
AGCTATGCTG	ATGAGGAAGA	AGCCAAAGTC	ATAACGTGGA	AAAAGATCGA	TCTCCCGTAC	540
GTCGAGGTAG	TTTCCAGCGA	GAGGGAGATG	ATAAAGCGGT	TCCTCAAAGT	GATAAGGGAG	600
AAAGATCCCG	ATGTTATAAT	TACCTACAAC	GGCGATTCTT	TCGACCTTCC	CTATCTAGTT	660
AAGAGGGCCG	AAAAGCTCGG	GATAAAGCTA	CCCCTGGGAA	GGGACGGTAG	TGAGCCAAAG	720
ATGCAGAGGC	TTGGGGATAT	GACAGCGGTG	GAGATAAAGG	GAAGGATACA	CTTTGACCTC	780
TACCACGTGA	TTAGGAGAAC	GATAAACCTC	CCAACATACA	CCCTCGAGGC	AGTTTATGAG	840
GCAATCTTCG	GAAAGCCAAA	GGAGAAAGTT	TACGCTCACG	AGATAGCTGA	GGCCTGGGAG	900
ACTGGAAAAG	GACTGGAGAG	AGTTGCAAAG	TATTCAATGG	AGGATGCAAA	GGTAACGTAC	960
GAGCTCGGTA	GGGAGTTCTT	CCCAATGGAG	GCCCAGCTTT	CAAGGTTAGT	CGGCCAGCCC	1020
CTGTGGGATG	TTTCTAGGTC	TTCAACTGGC	AAC TTGGTGG	AGTGGTACCT	CCTCAGGAAG	1080
GCCTACGAGA	GGAAATGAAT	GGCTCCAAAC	AAGCCGGATG	AGAGGGAGTA	CGAGAGAAGG	1140
CTAAGGGAGA	GCTACGCTGG	GGGATACGTT	AAGGAGCCGG	AGAAAGGGCT	CTGGGAGGGG	1200
TTAGTTTCCC	TAGATTTCAG	GAGCCTGTAC	CCCTCGATAA	TAATCACCCA	TAACGTCTCA	1260
CCGGATACGC	TGAACAGGGA	AGGGTGTAGG	GAATACGATG	TCGCCCCAGA	GGTTGGGCAC	1320
AAGTTCTGCA	AGGACTTCCC	GGGGTTTATC	CCCAGCCTGC	TCAAGAGGTT	ATTGGATGAA	1380
AGGCAAGAAA	TAAAAAGGAA	GATGAAAGCT	TCTAAAGACC	CAATCGAGAA	GAAGATGCTT	1440
GATTACAGGC	AACGGGCAAT	CAAAATCCTG	GCAAACAGCT	ATTATGGGTA	TTATGGGTAC	1500
GCAAAAGCCC	GTTGGTACTG	TAAGGAGTGC	GCAGAGAGCG	TTACGGCCTG	GGGAGGGGAA	1560
TATATAGAGT	TCGTAAGGAA	GGAACTGGAG	GAAAAGTTTCG	GGTTCAAAGT	CTTATACATA	1620
GACACAGATG	GACTCTACGC	CACAATTCCT	GGGGCAAAAC	CCGAGGAGAT	AAAGAAGAAA	1680
GCCCTAGAGT	TCGTAGATTA	TATAAACGCC	AAGCTCCCAG	GGCTGTTGGA	GCTTGAGTAC	1740
GAGGGCTTCT	ACGTGAGAGG	GTTCTTCGTG	ACGAAGAAGA	AGTATGCGTT	GATAGATGAG	1800
GAAGGGAAGA	TAATCACTAG	GGGGCTTGAA	ATAGTCAGGA	GGGACTGGAG	CGAAATAGCC	1860
AAAGAAACCC	AAGCAAAAGT	CCTAGAGGCT	ATCCTAAAGC	ATGGCAACGT	TGAGGAGGCA	1920
GTAAGAGATAG	TTAAGGAGGT	AACTGAAAAG	CTGAGCAAGT	ACGAAATACC	TCCAGAAAAG	1980
CTAGTTATTT	ACGAGCAGAT	CACGAGGCC	CTTCACGAGT	ACAAGGCTAT	AGGTCCGCAC	2040
GTTGCCGTGG	CAAAAAGGTT	AGCCGCTAGA	GGAGTAAAGG	TGAGGCCCTGG	CATGTTGATA	2100
GGGTACATAG	TGCTGAGGGG	AGACGGGCCA	ATAAGCAAGA	GGGCTATCCT	TGCAGAGGAG	2160

Replacement Figure

```
TTCGATCTCA GGAAGCATAA GTATGACGCT GAGTATTACA TAGAAAATCA GGTTTACCT 2220
GCCGTTCTTA GAATATTAGA GGCCTTTGGG TACAGGAAAG AAGACCTCAG GTGGCAGAAG 2280
ACTAAACAGA CAGGTCTTAC GGCATGGCTT AACATCAAGA AGAAG // 2328

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA // TGA
```

Figure 17BBB

Sac7d - Deep Vent DNA polymerase fusion protein

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 37)
Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 38)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA //

//ATGATACTTG ACGCTGACTA CATCACCGAG GATGGGAAGC CGATTATAAG GATTTTCAAG 60
AAAGAAAACG GCGAGTTTAA GGTGAGTAC GACAGAAACT TTAGACCTTA CATTTACGCT 120
CTCCTCAAAG ATGACTCGCA GATTGATGAG GTTAGGAAGA TAACCGCCGA GAGGCATGGG 180
AAGATAGTGA GAATTATAGA TGCCGAAAAG GTAAGGAAGA AGTTCCTGGG GAGGCCGATT 240
GAGGTATGGA GGCTGTACTT TGAACACCCCT CAGGACXXXC CCGCAATAAG GGATAAGATA 300
AGAGAGCATT CCGCAGTTAT TGACATCTTT GAGTACGACA TTCCGTTTCG GAAGAGGTAC 360
CTAATAGACA AAGGCCTAAT TCCAATGGAA GCGATGAAG AGCTCAAGTT GCTCGCATTT 420
GACATAGAAA CCCTCTATCA CGAAGGGGAG GAGTTCGCGA AGGGCCCAT TATAATGATA 480
AGCTATGCTG ATGAGGAAGA AGCCAAAGTC ATAACGTGA AAAAGATCGA TCTCCCGTAC 540
GTCGAGGTAG TTTCACGCGA GAGGGAGATG ATAAAGCGGT TCCTCAAGGT GATAAGGGAG 600
AAAGATCCCG ATGTTATAAT TACCTACAAC GCGATTCTT TCGACCTTCC CTATCTAGTT 660
AAGAGGGCCG AAAAGCTCGG GATAAAGCTA CCCCTGGGAA GGGACGGTAG TGAGCCAAAG 720
ATGCAGAGGC TTGGGGATAT GACAGCGGTG GAGATAAAGG GAAGGATACA CTTTGACCCTC 780
TACCACGTGA TTAGGAGAAC GATAAACCTC CCAACATACA CCTCGAGGC AGTTTATGAG 840
GCAATCTTCG GAAAGCCAAA GGAGAAAGTT TACGCTCAG AGATAGCTGA GGCCTGGGAG 900
ACTGGAAGG GACTGGAGAG AGTTGCAAAG TATTCAATGG AGGATGCAAA GGTAACGTAC 960
GAGCTCGGTA GGGAGTTCTT CCCAATGGAG GCCCAGCTTT CAAGGTTAGT CGGCCAGCCC 1020
CTGTGGGATG TTTCTAGGTC TTCAACTGGC AACTTGGTGG AGTGGTACCT CCTCAGGAAG 1080
GCCTACGAGA GGAATGAATT GGCTCCAAAC AAGCCGGATG AGAGGGAGTA CGAGAGAAGG 1140
CTAAGGGAGA GCTACGCTGG GGGATACGTT AAGGAGCCGG AGAAAGGGCT CTGGAGGGG 1200
TTAGTTTCCC TAGATTTTCA GAGCCTGTAC CCCTCGATAA TAATCACCCA TAACGTCTCA 1260
CCGGATACGC TGAACAGGGA AGGGTGTAGG GAATACGATG TCGCCCCAGA GGTGGGCAC 1320

Replacement Figure

AAGTTCTGCA AGGACTTCCC GGGGTTTATC CCCAGCCTGC TCAAGAGGTT ATTGGATGAA 1380
AGGCAAGAAA TAAAAAGGAA GATGAAAGCT TCTAAAGACC CAATCGAGAA GAAGATGCTT 1440
GATTACAGGC AACGGGCAAT CAAAATCCTG GCAAACAGCT ATTATGGTA TTATGGGTAC 1500
GCAAAAGCCC GTTGGTACTG TAAGGAGTGC GCAGAGAGCG TTACGGCCTG GGGAGGGAA 1560
TATATAGAGT TCGTAAGGAA GGAACCTGGAG GAAAGTTTCG GGTTCAAAGT CTTATACATA 1620
GACACAGATG GACTCTACGC CACAATTCCT GGGCAAAAC CCGAGGAGAT AAAGAAGAAA 1680
GCCCTAGAGT TCGTAGATTA TATAAACGCC AAGCTCCAG GGTGTTGGA GCTTGAGTAC 1740
GAGGGCTTCT ACGTGAGAGG GTTCTTCGTG ACGAAGAAGA AGTATGCGTT GATAGATGAG 1800
GAAGGGAAGA TAATCACTAG GGGGCTTGAA ATAGTCAGGA GGGACTGGAG CGAAATAGCC 1860
AAAGAAACCC AAGCAAAAGT CCTAGAGGCT ATCCTAAAGC ATGGCAACGT TGAGGAGGCA 1920
GTAAGATAG TTAAGGAGGT AACTGAAAAG CTGAGCAAGT ACGAAATACC TCCAGAAAAG 1980
CTAGTTATTT ACGAGCAGAT CACGAGGCC CTTACAGAGT ACAAGGCTAT AGTCCGCAC 2040
GTTGCCGTGG CAAAAGGTT AGCCGCTAGA GGAGTAAAGG TGAGGCCTGG CATGGTGATA 2100
GGGTACATAG TGCTGAGGG AGACGGCCA ATAAGCAAGA GGGCTATCCT TGCAGAGGAG 2160
TTCGATCTCA GGAAGCATAA GTATGACGCT GAGTATTACA TAGAAAATCA GGTTTTACCT 2220
GCCGTTCTTA GAATATTAGA GGCCTTTGGG TACAGGAAAG AAGACCTCAG GTGGCAGAAG 2280
ACTAAACAGA CAGGTCTTAC GGCATGGCTT AACATCAAGA AGAAG TAA 2328

Figure 17CCC

JDF-3 - Sac7d fusion protein

Nucleotide sequence (SEQ ID NO: 39) // Nucleotide sequence (SEQ ID NO: 69)
Nucleotide sequence (SEQ ID NO: 40) // Nucleotide sequence (SEQ ID NO: 69)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATCCTTGACGTTGATTACATCACCGAGAAATGGAAGCCCGTCATCAGGGTCTTCAAGAAGGAGAACGGCGAGTTCAGGATTGAATACGACCGGAGTTCGAGCCCTACTTCT
ACGGCTCCTCAGGGACGACTCTGCCATCGAAGAAATCAAAAGATAACCGGGAGAGGCACGGCAGGTCGTTAAGGTTAAGCGCGGAGAGGTGAAGAAAAAGTTCCCTCGG
CAGGTCTGTGAGGTCGTGGTCCCTACTTACGCACCCCGCAGGACXXXCCGGCAATCCGCGACAAAATAAGGAAGCACCCCGGTCTATCGACATCTACGAGTACGACATACCC
TTCGCCAAGCGTACCTCATAGACAAAGGGCCTAATCCGATGGAAGGTGAGGAAGAGCTTAAACTCATGTCTTGGATCGAGACGCTCTACCCACGAGGGAGAAAGATTGGAA
CCGGGCCGATTCTGATGATAAGCTACGCCGATGAAAGCGAGCGCGGTGATAACCTGGAAGAAGATCGACCTTCTTACGTTGAGGTTGTCTCCACCGAGAAGGAGATGATTAA
GCGCTTCTTGAGGTCGTTAAGGAGAAAGGACCCGGACGTGCTGATAACATACGCGACAACTTCGACTTCGCCCTACCTGAAAAAGCGCTGTGAGAAAGCTTGGCGTGAGCTTT
ACCCTCGGGAGGACGGGAGCGGAGCCGAAGATACAGCGCATGGGGACAGGTTTTCGGTCGAGGTGAAGGCGAGGTCACCTTCGACCTTTATCCAGTCATAAGGCGCACCATAA
ACCTCCGACCTACACCCCTTGAGGCTGTATACGAGGCGGTTTTCGGCAAGCCCAAGGAGAAGGTCTACGCCGAGGAGATAGCCACCGCTGGGAGACCGGCGGCTTGAGAG

GGTCGCGGCTACTCGATGGAGGACGCGAGGGTTACCTACGAGCTTGGCAGGGAGTTCTTCCGATGGAGGCCAGCTTTCAGGCTCATCGGCCAAGGCCTCTGGGACGTTTCC
CGCTCCAGCACCGGCAACCTCGTCGAGTGTTCTCTTAAGGAAGCCCTACGAGAGGAACGAACTCGCTCCCAACAAGCCCGACGAGAGGAGCTGGCGAGGAGAAGGGGGCT
ACGCGGTGGCTACGTCAAGGAGCCGGAGCGGGACTGTGGACAATATCGTGATCTAGACTTTCGTAGTCTCTAC[CCT]TCAATCATATACCCACAAACGTCTCGCCAGATAC
GCTCAACCGGAGGGGTAGGAGCTACGACGTTGCCCGGAGGTCGATCAAGTTCTGCAAGGACTTCCCCGGCTTCATTCCGAGCCTGCTCGGAAACCTGCTGGAGGAAAGG
CAGAAGATAAGAGGAAGATGAAGCAACTCTCGACCCGCTGGAGAAGAAATCTCCTCGATTACAGGCAACG[GCC]ATCAAGATTCTCGCCAACAGCTACTACGGCTACTACGGCT
ATGCCAGGGCAAGATGGTACTGTCAGGGAGTGCCCGAGAGCGTTACGGCATGGGAAGGAGTACATCGAAATGGTCAATCAGAGAGCTTGAGGAAAGTTTCGGTTTAAAGTCCT
CTATGCAGACACAGACGGTCTCCATGCCACCATTCCTGGAGCGGACGCTGAACACAGTCAAGAAAAGGCAATGGAGTTCTTAAACTATATCAATCCCAAACTGCCCGCCTTCTC
GAACTCGAATACGAGGGCTTCTACGTACGGGCTTCTTTCGTACGAAGAAAGTAACGGGTCAATCGACGAGGGCAAGATAACACCGCGGGCTTGAGATAGTCAGGCGCG
ACTGGAGCGAGATAGCGAAGGAGACGCGAGCGGTTTGGAGGCGATACTCAGGCACGGTGACGTTGAAGAGGCCGTCAGAAATTGTCAGGGAAGTACCCGAAAAGCTGAGCAA
GTACGAGGTTCCCGGAGAAAGCTGGTTATCCACGAGCAGATAAACGGCGGAGCTCAAGGACTACAAAGCCACCGGCTAGCCATAGCCATAGCGAAGCGTTTGCGCCCGCAGAGGT
GTTAAATCCGGCCCCGGAACGTGTGATAAGCTACATCGTTCTGAAGGCTCCGGAAGGATAGGCGACAGGGCGATTCCCTTCGACGAGTTTCGACCCGACGAAAGCACAAAGTACGATG
CGGACTACTACATCGAGAACCGAGTTCTGCCGCGCAGTTGAGAGAAATCCTCAGGGCTTTCGGCTACCGCAAGGAAGACCTGCGCTACCAGAAAGACGAGGCAGGCTTGGCGC
GTGGCTGAAGCCGAAGGGGAAGAAAG//

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
TTA GAC ATG TTA GCA AGA GCA GAA AAG AAA // TAG

Figure 17DDD

Sac7d - JDF-3 fusion protein

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 39)
Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 40)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
TTA GAC ATG TTA GCA AGA GCA GAA AAG AAA //

Replacement Figure

//ATGATCCTTGACGTTGATTACATCACCGAGAAATGAAAGCCCGTCAATCAGGGTCTTCAAGAAGGAGAACGGCGAGTTCAGGATTGAATACGACCGCGAGTTCGAGCCCTACTTCTACCGGCTCCTCAGGGACGACTCTGTCCATCGAAGAAATCAAAAAGATAAACCGCGAGAGGCACGGCAGGGTCGTTAAGGTTAAGCGCGGAGAGGTGAAGAAAAGTTCCCTCAGAGGTCGTGGAGGTCCTCTACTTCAACGACCCGAGACXXXCCGGCAATCCCGGACAATAAGGAAGCACCCTGGTCAATCGACATCTACGAGTACGACATACCTTCGCCAAGCGCTACCTCATAGACAAGGCCCTAATCCCAGATGGAAGGTGAGGAAGCTTAAACTCATGTCTTCGACATCGAGACGCTCTACCGAGGGAGAGAGTTTGAACCGGGCCGATTCTGATGATAAGCTACGCCGATGAAGCGAGCGCGTGATAACCTGGAAGAAGATCGACCTTCCTTACGTTGAGTTGTCTCCACCGAGAAAGGAGATGATTAAAGCGCTTCTTGAGGTCGTTAAGGAGAAGACCCGACGTGCTGATAACATACAACGGCGACAACCTTCGACTTCGCCCTACCTGAAAAAGCGCTGTGAGAAAGCTTGGCGTGAGCTTTACCCCTCGGAGGACCGGAGCGAGCCGAAGATACAGCGCATGGGGACAGGTTTTCGGTCGAGGTGAAGGCGAGGTACACTTCGACCTTTATCCAGTCAATAAGGCGCACCATAAACCTCCGACCTACACCTTGAGGCTGTATACGAGCGGTTTTTCGGCAAGCCCAAGGAGAGGTCTACGCCGAGGAGATAGCCACCGCTGGGAGACCGGCGAGGGCTTGAGAGGTCGCGCTACTCGATGGAGACGCGAGGTTACCTACGAGCTTGGCAGGAGTTCTTCCGATGGAGGCCAGCTTTCAGGCTCATCGGCCAAGGCCCTCTGGGACGTTTCCGCTCCAGCACCGGCAACCTCGTCGAGTGGTTCCCTCAAGGAAGCCTACGAGAGGAACGAACCTCGCTCCCAACAAGCCCGACGAGAGGAGCTGGCGAGGAGAAAGGGGGCTACGCTCAAGGAGCCGGAGCGGGGACTGTGGACAATATCGTGATCTAGACTTTCGTAGTCTCTACCCCTCAATCATAATCACCCACAACGTCTCGCCAGATACGCTCAACCGGAGGGGTAGGAGCTACGACGTTGCCCGGAGGTCACAAAGTTCTGCAAGGACTTCCCCTTCATTCCGAGCCTGTCTGGAAACCTGCTGGAGGAAAAGCAGAGAATAAGAGGAAGATGAAGGCAACTCTCGACCCGAGAGTCCGCGATGGGAAGGAGTACATCGAAATGGTCAATCAGAGAGCTTGAGGAAAAGTTCGGTTTAAAGTCTATGACAGACACAGACGGTCTCCATGCCCACCATTCCTGGAGCGGACGCTGAACAGTCAAGAAAAAGCAATGGAGTCTTAAACTATATCAATCCCAAACCTGCCCGCTTCGAACTCGAATACGAGGGCTTCTACGTCAGGGCTTCTACGTCAGGGCTTCTCGTCAAGGAGACGAGGCGAGGGTTTTTGGAGGCGATACTCAGGCACGGTGACGTTGAAGAGCCGTCAAGATTGTCAAGGAAGTCACCGAAAAGCTGAGCAAGTACGAGGTTCGGCCGGAGAAGCTGGTTATCCACGAGCAGATAACGCGCAGCTCAAGGACTACAAGGCCACCGGCCCTAGCCATAGCCGAAGCGTTTGGCCCGCAGAGGTGTTAAATCCGGCCCGGAACGTGTGATAAGCTACATCGTTCTGAAGGCTCCGGAAGGATAGGCGACAGGGCATTCCTTCGACGAGTTTCGACCCGACGAAAGCACAAGTACGATGCGGACTACTACATCGAGAACCAAGTTCTGCGCGCAGTTGAGAGAAATCCTCAGGGCCTTCGGCTACCGGCAAGGAGGAGGCAAGGAGTGA

Replacement Figure

Figure 17EEE

Synthetic Sso7d gene:

Nucleotide sequence (SEQ ID NO: 71)

Amino acid sequence (SEQ ID NO: 72)

```
A   T   V   K   F   K   Y   K   G   E   E   K   E   V   D   I   S   K
GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG

I   K   K   V   W   R   V   G   K   M   I   S   F   T   Y   D   E   G
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC

G   G   K   T   G   R   G   A   V   S   E   K   D   A   P   K   E   L
GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG

L   Q   M   L   E   K   Q   K   K
CTG CAG ATG CTG GAG AAG CAG AAA AAG
```

Figure 17FFF

Sso7d-Taq DNA polymerase fusion protein

Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 65)

Amino acid sequence (SEQ ID NO: 72) // Amino acid sequence (SEQ ID NO: 66)

```
// A   T   V   K   F   K   Y   K   G   E   E   K   E   V   D   I   S   K
// GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG

I   K   K   V   W   R   V   G   K   M   I   S   F   T   Y   D   E   G
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC

G   G   K   T   G   R   G   A   V   S   E   K   D   A   P   K   E   L
GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG

L   Q   M   L   E   K   Q   K   K   //   G   G   G
CTG CAG ATG CTG GAG AAG CAG AAA AAG   //   GGC GGC GGT
```

Replacement Figure

V T S G M L L P L F E P K G R V L L L V
GTC ACT AGT GGG ATG CTG CCC CTC TTT GAG CCC AAG GGC CGG GTC CTC CTG GTG

D G H H L A Y R T F H A L K G L T T
GAC GGC CAC CAC CTG GCC TAC CGC ACC TTC CAC GCC CTG AAG GGC CTC ACC ACC

S R G E P V Q A V Y G F A K S L L K
AGC CGG GGG GAG CCG GTG CAG GCG GTC TAC GGC TTC GCC AAG AGC CTC CTC AAG

A L K E D G D A V I V F D A K A P
GCC CTC AAG GAG GAC GGG GAC GCG GTG ATC GTG GTC TTT GAC GCC AAG GCC CCC

S F R H E A Y G G Y K A G R A P T P
TCC TTC CGC CAC GAG GCC TAC GGG GGG TAC AAG GCG GGC CGG GCC CCC ACG CCA

E D F P R Q L A L I K E L V D L L G
GAG GAC TTT CCC CGG CAA CTC GCG CTC ATC AAG GAG CTG GTG GAC CTC CTG GGG

L A R L E V P G Y E A D D V L A S L
CTG GCG CGC CTC GAG GTC CCG GCG TAC GAG GCG GAC GAC GTC CTG GCC AGC CTG

A K K A E K E G Y E V R I L T A D K
GCC AAG AAG GCG GAA AAG GAG GGC TAC GAG GTC CGC ATC CTC ACC GCC GAC AAA

D L Y Q L L S D R I H V L H P E G Y
GAC CTT TAC CAG CTC CTT TCC GAC CGC ATC CAC GTC CTC CAC CCC GAG GGG TAC

L I T P A W L W E K Y G L R P D Q W
CTC ATC ACC CCG GCC TGG CTT TGG GAA AAG TAC GGC CTG AGG CCC GAC CAG TGG

A D Y R A L T G D E S D N L P G V K
GCC GAC TAC CGG GCC CTG ACC GGG GAC GAG TCC GAC AAC CTT CCC GGG GTC AAG

G I G E K T A R K L L E E W G S L E
GGC ATC GGG GAG AAG ACG GCG AGG AAG CTT CTG GAG GAG TGG GGG AGC CTG GAA

A L L K N L D R L K P A I R E K I L
GCC CTC CTC AAG AAC CTG GAC CGG CTG AAG CCC GCC ATC CGG GAG AAG ATC CTG

A H M D D L L K L S W D L A K V R T D

GCC CAC ATG GAC GAT CTG AAG CTC TCC TGG GAC CTG GCC AAG GTG CGC ACC GAC
L P L E V D F A K R R E P D R E R L
CTG CCC CTG GAG GTG GAC TTC GCC AAA AGG CGG GAG CCC GAC CGG GAG AGG CTT
R A F L E R L E F G S L L H E F G L
AGG GCC TTT CTG GAG AGG CTT GAG TTT GGC AGC CTC CTC CAC GAG TTC GGC CTT
L E S P K A L E E A P W P P E G A
CTG GAA AGC CCC AAG GCC CTG GAG GAG GCC CCC TGG CCC CCG CCG GAA GGG GCC
F V G F V L S R K E P M W A D L L A
TTC GTG GGC TTT GTG CTT TCC CGC AAG GAG CCC ATG TGG GCC GAT CTT CTG GCC
L A A A R G G GGC CGG GTC CAC CGG GCC CCC GAG CCT TAT AAA GCC
CTG GCC GCC AGG AGG GGC CTT GGC CTC CCG CCC GGC GAC CCC ATG CTC CTC GCC
L R D L K E A R G L L A K D L S V L
CTC AGG GAC CTG AAG GAG GCG CGG GGG CTT CTC GCC AAA GAC CTG AGC GTT CTG
A L R E G L G L P P G D D P M L L A
GCC CTG AGG GAA GGC CTT GGC CTC CCG CCC GGC GAC GAC CCC ATG CTC CTC GCC
Y L L D P S N T T P E G V A R R Y G
TAC CTC CTG GAC CCT TCC AAC ACC ACC CCC GAG GGG GTG GCC CGG CGC TAC GGC
G E W T E E A G E R A A L S E R L F
GGG GAG TGG ACG GAG GAG GCG GGG GAG CGG GCC CTT TCC GAG AGG CTC TTC
A N L W G R L E G E E R L L W L Y R
GCC AAC CTG TGG GGG AGG CTT GAG GGG GAG AGG CTC CTT TGG CTT TAC CGG
E V E R P L S A V L A H M E A T G V
GAG GTG GAG AGG CCC CTT TCC GCT GTC CTC GGC CAC ATG GAG GCC ACG GGG GTG
R L D V A Y L R A L S L E V A E I
CGC CTG GAC GTG GCC TAT CTC AGG GCC TTG TCC CTG GAG GTG GCC GAG GAG ATC
A R L E A E V F R L A G H P F N L N
GCC CGC CTC GAG GCC GAG GTC TTC CGC CTG GCC CAC CCC TTC AAC CTC AAC

S R D Q L E R V L F D E L G L P A I
TCC CGG GAC CAG CTG GAA AGG GTC CTC TTT GAC GAG CTA GGG CTT CCC GCC ATC

G K T E K T G K R S T S A A V L E A
GGC AAG ACG GAG AAG ACC GGC AAG CGC TCC ACC AGC GCC GTC CTG GAG GCC

L R E A H P I V E K I L Q Y R E L T
CTC CGC GAG GCC CAC CCC ATC GTG GAG AAG ATC CTG CAG TAC CGG GAG CTC ACC

K L K S T Y I D P L P D L I H P R T
AAG CTG AAG AGC ACC TAC ATT GAC CCC TTG CCG GAC CTC ATC CAC CCC AGG ACG

G R L H T R F N Q T A T A T G R L S
GGC CGC CTC CAC ACC CGC TTC AAC CAG ACG GCC ACG GCC AGG CTA AGT

S S D P N L Q N I P V R T P L G Q R
AGC TCC GAT CCC AAC CTC CAG AAC ATC CCC GTC CGC ACC CCG CTT GGG CAG AGG

I R R A F I A E E G W L L V A L D Y
ATC CGC CGG GCC TTC ATC GCC GAG GAG GGG TGG CTA TTG GTG GCC CTG GAC TAT

S Q I E L R V L A H L S G D E N L I
AGC CAG ATA GAG CTC AGG GTG CTG GCC CAC CTC TCC GGC GAC GAG AAC CTG ATC

R V F Q E G R D I H T E T A S W M F
CGG GTC TTC CAG GAG GGG CGG GAC ATC CAC ACG GAG ACC GCC AGC TGG ATG TTC

G V P R E A V D P L M R R A A K T I
GGC GTC CCC CGG GAG GCC GTG GAC CCC CTG ATG CGC CGG GCC AAG ACC ATC

N F G V L Y G M S A H R L S Q E L A
AAC TTC GGG GTC CTC TAC GGC ATG TCG GCC CAC CGC CTC TCC CAG GAG CTA GCC

I P Y E E A Q A F I E R Y F Q S F P
ATC CCT TAC GAG GAG GCC CAG GCC TTC ATT GAG CGC TAC TTT CAG AGC TTC CCC

K V R A W I E K T L E E G R R R G Y
AAG GTG CGG GCC TGG ATT GAG AAG ACC CTG GAG GAG GGC AGG AGG CGG GGG TAC

V E T L F G R R Y V P D L E A R V
GTG GAG ACC CTC TTC GGC CGC CGC TAC GTG CCA GAC CTA GAG GCC CGG GTG

```
K  S  V  R  E  A  A  E  R  M  A  F  N  M  P  V  Q  G
AAG AGC GTG CGG GAG GAG GCG GCC GAG CGC ATG GCC TTC AAC ATG CCC GTC CAG GGC

T  A  A  D  L  M  K  L  A  M  V  K  L  F  P  R  L  E
ACC GCC GCC GAC CTC ATG AAG CTG GCT ATG GTG AAG CTC TTC CCC AGG CTG GAG

E  M  G  A  R  M  L  L  Q  V  H  D  E  L  V  L  E  A
GAA ATG GGG GCC AGG ATG CTC CTT CAG GTC CAC GAC GAG CTG GTC CTC GAG GCC

P  K  E  R  A  E  A  V  A  R  L  A  K  E  V  M  E  G
CCA AAA GAG AGG GCG GAG GCC GTG GCC CGG CTG GCC AAG GAG GTC ATG GAG GGG

V  Y  P  L  A  V  P  L  E  V  E  V  G  I  G  E  D  W
GTG TAT CCC CTG GCC GTG CCC CTG GAG GTG GAG GTG GGG ATA GGG GAG GAC TGG

L  S  A  K  E  G  I  D  G  R  G  G  G  H  H  H  H
CTC TCC GCC AAG GAG GGC ATT GAT GGC CGC GGA GGC GGC CAT CAT CAT CAT

H  H  *
CAT CAT TAA
```

Figure 17GGG

Pfu DNA Polymerase (WT) -Sso7d fusion protein

Nucleotide sequence (SEQ ID NO: 61) // Nucleotide sequence (SEQ ID NO: 71)

```
//
ccctggctct ggggccacat atatgttctt actgccttt atgaagaatc cccagtcgc
tctaacctgg gttatagtga caaatcttcc tccaccaccg cccaagaagg ttatttctat
caactctaca cctcccctat tttctctctt atgagatttt taagtatagt tatagagaag
gttttatact ccaaaactgag ttagtagata tgtggggagc ataatgattt tagatgtgga
```

Replacement Figure

ttacataact gaagaaggaa aacctgttat taggtattc aaaaaagaga acgaaaaatt
taagatagag catgatagaa cttttagacc atacatttac gctcttctca gggatgattc
aaagattgaa gaagttaaga aaataacggg gaaaaggcat ggaaagattg tgagaattgt
tgatgtagag aaggttgaga aaaagtttct cggcaagcct attaccgtgt ggaaacttta
tttggaacat cccaagatg tcccactat tagagaaaa gtagagaaac atccagcagt
tgtggacatc ttcgaatacg atattccatt tgcaaaagaga tacctcatcg acaaaggcct
aataccaatg gagggggaag aagagctaaa gattcttgcc ttcgatatag aaaccctcta
tcacgaagga gaagagttag gaaaaggccc aattataatg attagtatg cagatgaaaa
tgaagcaaaag gtgattactt ggaaaaacat agatcttcca tacgttgagg ttgtatcaag
cgagagagag atgataaaga gatttctcag gattatcagg gagaaggatc ctgacattat
agttacttat aatggagact cattcgactt ccatattta gcgaaaaggg cagaaaaact
tgggattaaa ttaaccattg gaagagatgg aagcgagccc aagatgcaga gaataggcga
tatgacggct gtagaagtca agggaagaat acatttcgac ttgtatcatg taataacaag
gacaataaat ctccaacat acacactaga ggctgtatat gaagcaattt ttggaaagcc
aaaggagaag gtatacgccg acgagatagc aaaagcctgg gaaagtggag agaaccctga
gagagttgcc aaatactcga tggaagatgc aaaggcaact tatgaactcg ggaaagaatt
ccttccaatg gaaattcagc tttcaagatt agttggacaa cctttatggg atgtttcaag
gtcaagcaca gggaaccttg tagagtgggtt ctacttagg aaagcctacg aaagaaacga
agtagctcca acaagccaa gtgaagagga gtatcaaaga aggctcaggg agagctacac
agggtggattc gttaaagagc cagaaaaagg gtgtgtggaa aacatagtat acctagattt
tagagcccta tatccctcga ttataattac ccacaatgtt tctccgata ctctaatct

Replacement Figure

tgagggatgc aagaactatg atatcgctcc tcaagtaggc cacaagttct gcaaggacat
ccctgggtttt ataccaagtc tcttgggaca tttgttagag gaaagacaaa agattaagac
aaaaatgaag gaaactcaag atcctataga aaaaatactc cttgactata gacaaaaagc
gataaaaactc ttagcaaatc ctttctacgg atattatggc tatgcaaaaag caagatggta
ctgtaaggag tgtgctgaga gcgttactgc ctggggaaga aagtacatcg agttagtatg
gaaggagctc gaagaaaaagt ttggatttaa agtcctctac attgacactg atggtctcta
tgcaactatc ccaggaggag aaagtgagga aataaagaaa aaggctctag aatttgtaaa
atacataaat tcaaagctcc ctggactgct agagcttgaa tatgaagggt ttataagag
gggattcttc gttacgaaga agaggtatgc agtaatagat gaagaaggaa aagtcattac
tcgtgggtta gagatagtta ggagagatg gagtgaaatt gcaaaaagaaa ctcaagctag
agttttggag acaatactaa aacacggaga tgttgaagaa gctgtgagaa tagtaaaaga
agtaatacaa aagcttgcca attatgaaat tccaccagag aagctcgcaa tatatgagca
gataacaaga ccattacatg agtataaggc gataggctct cacgtagctg ttgcaaaagaa
actagctgct aaaggagtta aaataaagcc aggaatggta attggataca tagtacttag
aggcgatggt ccaattagca atagggcaat tctagctgag gaatacgatc ccaaaaagca
caagtatgac gcagaatatc acattgagaa ccaggttctt ccagcggtag ttaggatatt
ggagggattt ggatacagaa aggaagacct cagataccaa aagacaagac aagtcggcct
aacttcctgg cttaacatta aaaatccta gaaaagcgat agatatcaac ttttattctt
tctaaccctt ttctatgaaa gaagaactga gcaggaatta ccagttcttc cgttatttta
tgggtaatta aaaacccatg ctcttgggag aatcttcgaa taaaatccct aacttcaggc

Replacement Figure

```
tttgctaagt gaatagaata aacaacatca ctcaattcaa acgccttcgt tagaaatggg
ctatctgcat gcttctcttg ctcggaann gaggattcat aacaacagta tcaacattct
cagagaattg agaaacatca gaaactttga cttctacaac atttctaact ttgcaactct
tcaagatttt ctaaaagaat tttaacggcc tcctcgtcaa ttctgacgac gtagatcttt
tttgctccaa gcagagccgc tccaatggat aacacccctg ttcccgccacc caagtccgct
acaatttttt ccttgtatct cctaattgtat aagcaagcca aaggagagta gatgctacct
ttccgggagt tttgtattgc tctagccaag gtttgggatt tttgaatcct ttaactctgg
aaagtataat ttcaagctcc ttcttcttca tgacagatga aaaattgttt tgtctctttt
taacttttac agaaataaact gtctcaaatt atgacaaactc ttgacatttt tacttcatta
ccagggtaat gttttttaagt atgaaatttt tctttcatag aggaggnnnn nngtcctctc
ctcgatttcc ttggttgctgc tccatatgat aagcttccaa agtgggtgtt cagactttta
gacactcaaa taccagacga caatgggtgt ctcaactcaag ccccatatgg gttgagaaaa
gtagaagcgg cactactcag atgcttcccc aggaatgagg ttgttgtagc tcntcccnga
aagattgaga tgttcttg //

// GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
CTG CAG ATG CTG GAG AAG CAG AAA AAG // TGA
```


Figure 17HHH

PFU DNA POLYMERASE (V93 R OR E) -Sso7d fusion protein

Nucleotide sequence (SEQ ID NO: 27) // Nucleotide sequence (SEQ ID NO: 71)

Nucleotide sequence (SEQ ID NO: 28) // Nucleotide sequence (SEQ ID NO: 71)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
ATGATTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTACGCT 120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAA TAACGGGGA AAGCATGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATXXC CCACTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCCTC 420
GATATAGAAA CCTTCTATCA CGAAGGAGAA GAGTTTGGA AAGGCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAATGA AGCAAAAGGTG ATTACTTGG AACAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCT ATATTAGCG 660
AAAAGGCAG AAAAAGTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAA AGCCTGGGA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAA GGCAACTTAT 960
GAACTCGGA AAGAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140
CTCAGGGAGA GCTACACAGG TGGATTTCGT AAAGAGCCAG AAAAGGGGT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCCT TCTACGGATA TTATGGCTAT 1500
GCAAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTAAGGAGG GGAAGAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680

Replacement Figure

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GCTCTAGAAT TTGTAAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGA AATTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAAATAG TAAAAGAAGT AATACAAAAG CTTGCCAAAT ATGAAATTCC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGC AATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTCTCTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280
ACAAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAATA AATCC 2328
// GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
CTG CAG ATG CTG GAG AAG CAG AAA AAG // TGA

```

Figure 17III

PFU DNA POLYMERASE (G387P/V93R OR E) -Sso7d fusion protein

Nucleotide sequence (SEQ ID NO: 29) // Nucleotide sequence (SEQ ID NO: 71)

Nucleotide sequence (SEQ ID NO: 30) // Nucleotide sequence (SEQ ID NO: 71)

G387P Mutant (CCN is the codon for Proline where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

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ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAA 60
AAAGAGAACG GAAAATTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATXXXC CCCTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTCG AAAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420
GATATAGAAA CCTCTATCA CGAAGGAGAA GAGTTTGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAAATGA AGCAAAGGTG ATTACTTGGA AAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCT ATATTAGCG 660
AAAAGGGCAG AAAAACTTGG GATTAAATTA ACCATTGGA GAGATGGAAG CGAGCCCAAG 720

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Replacement Figure

ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTGG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
GAACTCGGGA AAGAATTCCT TCCAATGGAA ATTCAAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTA AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGAGTA TCAAAGAAGG 1140
CTCAGGGAGA GCTACACACC NGGATTTCGT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAA 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTATA CCAAGTCTCT TGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCCT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCCTG GGGAAGAAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAAG GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAATTTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCCAAT ATGAAATTCC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAA TAAAGCCAGG AATGGTAAT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGCAAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTCTTTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTGGA TACAGAAAAG AAGACCTCAG ATACCAAAAAG 2280
ACAAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC // 2328

// GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
CTG CAG ATG CTG GAG AAG CAG AAA AAG // TGA

Figure 17JJJ

PFU DNA POLYMERASE (D141A/E143A/V93R OR E) - Sso7d fusion protein

Nucleotide sequence (SEQ ID NO: 31) // Nucleotide sequence (SEQ ID NO: 71)
Nucleotide sequence (SEQ ID NO: 32) // Nucleotide sequence (SEQ ID NO: 71)

Replacement Figure

D141A/E143A Mutant (GCN is the codon for alanine where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAA 60
AAAGAGAACG GAAAATTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATT TTTGAAATCCC CAAGATXXXC CCACATATTAG AGAAAAAGTT 300
AGAGAAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTCG AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420
GCNATAGCNA CCCCTCTATCA CGAAGGAGAA GAGTTTGGA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAAATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTTCC ATATTTAGCG 660
AAAAGGGCAG AAAAAGTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTGG GAAAGCCAAA GGAGAAAGTA TACGCCGACG AGATAGCAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAA GGCAACTTAT 960
GAACTCGGGA AAGAAATCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140
CTCAGGGAGA GCTACACA GTTGGATTCTGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAAATCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCCTG GGAAGAAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTT ATAAAGAGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAA TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAAATTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGCGGAT AGGTCTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAA TAAAGCCAGG AATGGTAAT 2100
GGATACATAG TACTTAGAG CGATGGTCCA ATTAGCAATA GGCATTTCT AGCTGAGGAA 2160
TAGGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAAACCA GGTCTTCCA 2220

Replacement Figure


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GCGGTACTTA GGATATTGGA GGGATTTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280
ACAAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC // 2328

// GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
CTG CAG ATG CTG GAG AAG CAG AAA AAG // TGA
```

Figure 17KKK

KOD DNA POLYMERASE - Sso7d fusion protein

Nucleotide sequence (SEQ ID NO: 33) // Nucleotide sequence (SEQ ID NO: 71)
Nucleotide sequence (SEQ ID NO: 34) // Nucleotide sequence (SEQ ID NO: 71)

```

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
ATGATCCTCG ACACTGACTA CATAACCGAG GATGAAAGC CTGTCAATAG AATTTCAAG 60
AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT TTGAACCCCTA CTTCTACGCC 120
CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAAAG TAACCGCCGA GAGCACGGG 180
ACGGTTGTAA CGGTTAAGCG GGTGAAAAG GTTCAGAAGA AGTTCCTCGG GAGACCAGTT 240
GAGGTCCTGA AACTCTACTT TACTCATCCG CAGGACXXXC CAGCGATAAG GGACAAAGATA 300
CGAGAGCATC CAGCAGTTAT TGACATCTAC GAGTACGACA TACCCCTTCG CAAGCGCTAC 360
CTCATAGACA AGGGATTAGT GCCAATGGAA GCGACGAGG AGCTGAAAAT GCTCGCCTC 420
GACATTGAAA CTCTCTACCA TGAGGGCGAG GAGTTCGCCG AGGGGCCAAT CCTTATGATA 480
AGCTACGCCG ACGAGGAAGG GGCCAGGGTG ATAACCTTGA AGAACGTGA TCTCCCTAC 540
GTTGACGTCG TCTCGACGGA GAGGGAGATG ATAAAGCGCT TCCTCCGTGT TGTGAAGGAG 600
AAAGACCCCG ACGTTCTCAT AACCTACAAC GCGACAAC TCGACTTCGC CTATCTGAAA 660
AAGCGCTGTG AAAAGCTCGG AATAAACTTC GCCCTCGGAA GGGATGGAAG CGAGCCGAAG 720
ATTCAGAGGA TGGGCGACAG GTTTGCCGTC GAAGTGAAG GACGGATACA CTTCGATCTC 780
TATCCTGTGA TAAGACGGAC GATAAACCTG CCACATACA CGCTTGAGGC CGTTTATGAA 840
GCCGTCTTCG GTCAGCCGAA GGAGAAGGTT TACGCTGAGG AAATAACCA AGCCTGGGA 900
ACCGGCGAGA ACCTTGAGAG AGTCGCCCGC TACTCGATGG AAGATGCGAA GGTCAATAC 960
GAGCTTGGGA AGGAGTTCCT TCCGATGGAG GCCCAGCTTT CTCGCTTAAT CGGCCAGTCC 1020
CTCTGGGACG TCTCCCGCTC CAGCACTGGC AACCTCGTTG AGTGGTTCTT CCTCAGGAAG 1080
GCCTATGAGA GGAATGAGCT GGCCCCGAAC AAGCCCGATG AAAGGAGCT GGCCAGAAGA 1140
CGGCAGAGCT ATGAAGGAGG CTATGTAAAA GAGCCCGAGA GAGGGTTGTG GGAGAACATA 1200
GTGTACCTAG ATTTTAGATC CCTGTACCCC TCAATCATCA TCACCCACAA CGTCTCGCCG 1260
GATACGCTCA ACAGAGAAGG ATGCAAGGAA TATGACGTTG CCCACAGGT CGGCCACCGC 1320
TTCTGCAAGG ACTTCCCAGG ATTTATCCCG AGCCTGCTTG GAGACCTCCT AGAGGAGAGG 1380
```

Replacement Figure

CAGAAGATAA AGAAGAAGAT GAAGGCCACG ATTGACCCGA TCGAGAGGAA GCTCCTCGAT 1440
TACAGGCAGA GGGCCATCAA GATCCTGGCA AACAGCTACT ACGTTACTA CGGCTATGCA 1500
AGGGCGCGCT GGTA CTGCAA GGAGTGCA GAGAGCGTAA CGGCTGGG AAGGAGTAC 1560
ATAACGATGA CCATCAAGGA GATAGAGGAA AAGTACGGCT TTAAGGTAAT CTACAGCGAC 1620
ACCGACGGAT TTTTGGCCAC AATACCTGGA GCCGATGCTG AAACCGTCAA AAAGAAAGGCT 1680
ATGGAGTTCC TCAAGTATAT CAACGCCAAA CTTCGGGCG CGCTTGAGCT CGAGTACGAG 1740
GGCTTCTACA AACCGGCTT CTTCGTCACG AAGAAGAAGT ATCGGTGAT AGACGAGGAA 1800
GGCAAGATAA CAACGCGCGG ACTTGAGATT GTGAGGCGTG ACTGGAGCGA GATAGCGAAA 1860
GAGACGCAGG CGAGGGTTCT TGAAGCTTGT CTAAAGGACG GTGACGTCGA GAAGGCCGTG 1920
AGGATAGTCA AAGAAGTTAC CGAAAAGCTG AGCAAGTACG AGGTTCCGCC GGAGAAAGCTG 1980
GTGATCCACG AGCAGATAAC GAGGGATTTA AAGGACTACA AGGCAACCGG TCCCCACGTT 2040
GCCGTTGCCA AGAGTTGGC CGCGAGAGGA GTCAAAATAC GCCCTGGAAC GGTGATAAGC 2100
TACATCGTGC TCAAGGGCTC TGGGAGGATA GCGACAGGG CGATACCGTT CGACGAGTTC 2160
GACCCGACGA AGCACAAGTA CGACGCCGAG TACTACATTG AGAACCAGGT TCTCCCAGCC 2220
GTTGAGAGAA TTCTGAGAGC CTTCGGTTAC CGCAAGGAAG ACCTGCGCTA CCAGAAAGACG 2280
AGACAGGTTG GTTTGAGTGC TTGGCTGAAG CCGAAGGGAA CT 2325

// GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
CTG CAG ATG CTG GAG AAG CAG AAA AAG // TGA

Figure 17LLL

Sso7d - KOD DNA POLYMERASE fusion protein

Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 33)

Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 34)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

//GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
CTG CAG ATG CTG GAG AAG CAG AAA AAG //

//ATGATCCTCG ACACTGACTA CATAACCGAG GATGGAAGC CTGTCAATAG AATTTCAAG 60
AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACCGACTT TTGAACCCCTA CTTCTACGCC 120
CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAAGA TAACCGCCGA GAGCACGGG 180
ACGGTTGTAA CGGTTAAGCG GGTGAAAAG GTTCAGAAAG AGTTCCTCGG GAGACCAGTT 240
GAGGTCTGGA AACTCTACTT TACTCATCCG CAGGACXXC CAGCGATAAG GGACAAGATA 300
CGAGAGCATC CAGCAGTTAT TGACATCTAC GAGTACGACA TACCCTTCGC CAAGCGCTAC 360
CTCATAGACA AGGGATTAGT GCCAATGGAA GCGACGAGG AGCTGAAAAT GCTCGCCTTC 420
GACATTGAAA CTCTCTACCA TGAGGGCGAG GAGTTCGCC AGGGCCCAAT CCTTATGATA 480
AGCTACGCCG ACGAGGAAGG GCCCAGGGTG ATAACTTGA AGAACGTGA TCTCCCCTAC 540
GTTGACGTCG TCTCGACGGA GAGGGAGATG ATAAAGCGCT TCCTCCGTGT TGTGAAGGAG 600
AAAGACCCGG ACGTTCTCAT AACCTACAAC GCGACAAC TCGACTTCGC CTATCTGAAA 660
AAGCGCTGTG AAAAGCTCGG AATAAACTTC GCCCTCGGAA GGGATGGAAG CGAGCCGAAG 720
ATTCAGAGGA TGGGCGACAG GTTTGCCGTC GAAGTGAAG GACGGATACA CTTCGATCTC 780
TATCCTGTGA TAAGACGGAC GATAAACCTG CCACATACA CGCTTGAGGC CGTTTATGAA 840
GCCGTCTTCG GTCAGCCGAA GGAGAAGGTT TACGCTGAGG AAATAACCAC AGCCTGGGAA 900
ACCGGCGAGA ACCTTGAGAG AGTCGCCCGC TACTCGATGG AAGATGCGAA GGTACACATAC 960
GAGCTTGGGA AGGAGTTCCT TCCGATGGAG GCCCAGCTTT CTCGCTTAAT CGGCCAGTCC 1020
CTCTGGGACG TCTCCCGCTC CAGCACTGGC AACCTCGTTG AGTGGTTCCT CCTCAGGAAG 1080
GCCTATGAGA GGAATGAGCT GGCCCGGAAC AAGCCGATG AAAAGGAGCT GGCCAGAAGA 1140
CGGCAGAGCT ATGAAGGAGG CTATGTAAAA GAGCCCGAGA GAGGGTTGTG GGAGAAACATA 1200
GTGTACCTAG ATTTTAGATC CCTGTACCCC TCAATCATCA TCACCCACAA CGTCTCGCCG 1260
GATACGCTCA ACAGAGAAGG ATGCAAGGAA TATGACGTTG CCCACAGGT CCGCCACCGC 1320
TTCTGCAAGG ACTTCCCAGG ATTTATCCCG AGCCTGCTTG GAGACCTCCT AGAGGAGAGG 1380
CAGAAGATAA AGAAGAAGAT GAAGGCCACG ATTGACCCGA TCGAGAGGAA GCTCCTCGAT 1440
TACAGGCAGA GGGCCATCAA GATCCTGGCA AACAGCTACT ACGTTACTA CGGCTATGCA 1500
AGGGCGCGCT GGTACTGCAA GGAGTGTGCA GAGAGCGTAA CCGCCTGGGG AAGGGAGTAC 1560
ATAACGATGA CCATCAAGGA GATAGAGGAA AAGTACGGCT TTAAGGTAAT CTACAGCGAC 1620
ACCGACGGAT TTTTGGCCAC AATACCTGGA GCCGATGCTG AAACCGTCAA AAAGAAGGCT 1680
ATGGAGTTCC TCAAGTATAT CAACGCCAAA CTTCGGGCG CGCTTGAGCT CGAGTACGAG 1740
GGCTTCTACA AACCGGCTT CTTCGTCACG AAGAAGAAGT ATGCGGTGAT AGACGAGGAA 1800
GGCAAGATAA CAACGCGCGG ACTTGAGATT GTGAGGCGTG ACTGGAGCGA GATAGCGAAA 1860
GAGACGCAGG CGAGGGTTCT TGAAGCTTTG CTAAAGGACG GTGACGTCGA GAAGGCCGTG 1920
AGGATAGTCA AAGAAGTTAC CGAAAAGCTG AGCAAGTACG AGTTCCGCC GGAGAAAGCTG 1980
GTGATCCACG AGCAGATAAC GAGGATTTA AAGGACTACA AGGCAACCGG TCCCCACGTT 2040
GCCGTTGCCA AGAGGTTGGC CGCGAGAGGA GTCAAAATAC GCCCTGGAAC GGTGATAAGC 2100
TACATCGTGC TCAAGGGCTC TGGGAGGATA GCGCACAGGG CGATACCGTT CGACGAGTTC 2160
GACCCGACGA AGCACAAGTA CGACGCCGAG TACTACATTG AGAACAGGT TCTCCAGCC 2220
GTTGAGAGAA TTCTGAGAGC CTTGCGTTAC CGCAAGGAAG ACCTGCGCTA CCAGAAGACG 2280
AGACAGGTTG GTTTGAGTGC TTGGCTGAAG CCGAAGGGAA CT //TAG 2325

Figure 17MMM

Sso7d-Vent DNA POLYMERASE FUSION PROTEIN

Nucleotide sequence (SEQ ID NO: 71) //Nucleotide sequence (SEQ ID NO: 35)

Nucleotide sequence (SEQ ID NO: 71) //Nucleotide sequence (SEQ ID NO: 36)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)

V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

//GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
CTG CAG ATG CTG GAG AAG CAG AAA AAG //

ATGATACTGG ACACTGATTA CATAACAAAA GATGGCAAGC CTATAATCCG AATTTTAAAG 60
AAAGAGAACG GGGAGTTTAA AATAGAACTT GACCCCTCAT TTCAGCCCTA TATATATGCT 120
CTTCTCAAAG ATGACTCCGC TATTGAGGAG ATAAAGGCAA TAAAGGCGA GAGACATGGA 180
AAAACTGTGA GAGTGCTCGA TGCAGTGAAG GTCAGGAAAA AATTTTGGG AAGGGAAGTT 240
GAAGTCTGGA AGCTCATTTT CGAGCATCCC CAAGACXXXC CAGCTATGCG GGGCAAAATA 300
AGGGAACATC CAGCTGTGGT TGACATTTAC TACCCTTTGC CAAGCGTTAT 360
CTCATAGACA AGGCTTTGAT TCCCATGGAG GGAGACGAGG AGCTTAAGCT CCTTGCCCTT 420
GATATTGAAA CGTTTATCA TGAGGGAGAT GAATTTGGAA AGGCGAGAT AATAATGATT 480
AGTTATGCCG ATGAAGAAGA GGCCAGAGTA ATCACATGGA AAAATATCGA TTTGCCGTAT 540
GTCGATGTTG TGTCCAATGA AAGAGAAATG ATAAAGCGTT TTGTTCAAGT TGTTAAAGAA 600
AAAGACCCCG ATGTGATAAT AACTTACAAT GGGACAATT TTGATTGCC GTATCTATA 660
AAACGGGCAG AAAAGCTGGG AGTTCGGCTT GTCTTAGGAA GGGACAAAGA ACATCCCGAA 720
CCCAAGATTG AGAGGATGGG TGATAGTTT GCTGTGAAA TCAAGGAGT AATCCACTTT 780
GATCTTTTCC CAGTTGTGCG AAGGACGATA AACCTCCCAA CGTATACGCT TGAGGCAGTT 840
TATGAAGCAG TTTTAGGAAA AACCAAAAGC AAATTAGGAG CAGAGGAAAT TGCCGCTATA 900
TGGGAAACAG AAGAAAGCAT GAAAAAATA GCCCAGTACT CAATGGAAGA TGCTAGGGCA 960
ACGTATGAGC TCGGGAAGGA ATTCTTCCCC ATGGAAGCTG AGCTGGCAA GCTGATAGGT 1020
CAAAAGTGAT GGGACGTCTC GAGATCAAGC ACCGGCAACC TCGTGGAGTG GTATCTTTTA 1080
AGGGTGGCAT ACGCGAGGAA TGAAC TTGCA CCGAACAAAC CTGATGAGGA AGAGTATAAA 1140
CGGCGCTTAA GAACAACCTTA CCTGGGAGGA TATGTAAAAG AGCCAGAAAA AGGTTTGTGG 1200
GAAAATATCA TTTATTTTGA TTTCCGCAGT CTGTACCCCTT CAATAATAGT TACTCACAA 1260
GTATCCCCAG ATACCCTTGA AAAAGAGGGC TGTAAGAAAT ACGATGTTGC TCCGATAGTA 1320
GGATATAGGT TCTGCAAGGA CTTTCCGGGC TTTATTCCCT CCATACTCGG GGACTTAATT 1380
GCAATGAGGC AAGATATAAA GAAGAAAAATG AAATCCACAA TTGACCCGAT CGAAAAAGAA 1440

Replacement Figure

ATGCTCGATT ATAGGCAAAG GGCTATTAAA TTGCTTGCAA ACAGCTATTA CGGCTATATG 1500
GGGTATCCTA AGGCAAGATG GTACTCGAAG GAATGTGCTG AAAGCGTTAC CGCATGGGG 1560
AGACACTACA TAGAGATGAC GATAAGAGAA ATAGAGGAAA AGTTCGGCTT TAAGGTTCTT 1620
TATGCGGACA CTGACGGCTT TTATGCCACA ATACCCGGGG AAAAGCCTGA ACTCATTAA 1680
AAGAAAGCCA AGGAATTCCCT AAACCTACATA AACTCCAAC TTCCAGGTCT GCTTGAGCTT 1740
GAGTATGAGG GCTTTTACTT GAGAGGATTC TTGTGTACAA AAAAGCGCTA TGCAGTCATA 1800
GATGAAGAGG GCAGGATAAC AACAGGGGC TTGGAAGTAG TAAAGGAGAG TTGGAGTGAG 1860
ATAGCTAAGG AGACTCAGG AAAGGTTTGA GAGGCTATAC TTAAAAGAGG AAGTGTTGAA 1920
AAAGCTGTAG AAGTTGTTAG AGATGTTGTA GAGAAATAG CAAAATACAG GGTTCACACT 1980
GAAAAGCTTG TTATCCATGA GCAGATTACC AGGGATTAA AGGACTACAA AGCCATTGGC 2040
CCTCATGTGC CGATAGCAAA AAGACTTGCC GCAAGAGGA TAAAAGTGAA ACCGGGCACA 2100
ATAATAAGCT ATATCGTTCT CAAAGGGAGC GAAAGATAA GCGATAGGT AATTTTACTT 2160
ACAGAAATACG ATCCTAGAAA ACACAAGTAC GATCCGGACT ACTACATAGA AAACCAAGTT 2220
TTGCCGGCAG TACTTAGGAT ACTCGAAGCG TTGTGATACA GAAAGGAGGA TTTAAGGTAT 2280
CAAAGCTCAA AACAAACCGG CTTAGATGCA TGGCTCAAGA GGTAG 2325

Figure 17NNN

Vent DNA POLYMERASE - Sso7d FUSION PROTEIN

Nucleotide sequence (SEQ ID NO: 35) // Nucleotide sequence (SEQ ID NO: 71)

Nucleotide sequence (SEQ ID NO: 36) // Nucleotide sequence (SEQ ID NO: 71)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)

V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATACTGG ACAC TGATTA CATAACAAA GATGGCAAGC CTATAATCCG AATTTTAAAG 60
AAAGAGAACG GGGAGTTTAA AATAGAACTT GACCTCTATT TTCAGCCCTA TATATATGCT 120
CTTCTCAAAG ATGACTCCGC TATTGAGGAG ATAAAGGCAA TAAAGGGCGA GAGACATGGA 180
AAAACGTGTA GAGTGCTCGA TGCAGTGAAA GTCAGGAAAA AATTTTGGG AAGGGAAGTT 240
GAAGTCTGGA AGCTCATTTT CGAGCATCCC CAAGACXXC CAGCTATGCG GGC AAAATA 300
AGGGAACATC CAGCTGTGGT TGACATTTAC GAATATGACA TACCCTTTGC CAAGCGTTAT 360
CTCATAGACA AGGCTTGAT TCCCATGGAG GGAGACGAGG AGCTTAAGCT CCTTGCCTTT 420
GATATTGAAA CGTTTATCA TGAGGGAGAT GAATTTGGA AGGCGAGAT AATAATGATT 480
AGTTATGCCG ATGAAGAAGA GGCCAGAGTA ATCAGATGGA AAAATATCGA TTTGCCGTAT 540
GTCGATGTTG TGTCCAATGA AAGAGAAATG ATAAAGCGTT TTGTTCAAGT TGTTAAAGAA 600
AAAGACCCCG ATGTGATAAT AACTTACAAT GGGACAATT TTGATTGCC GTATCTATA 660
AAACGGGCAG AAAAGCTGGG AGTTCGGCTT GTCTTAGGAA GGGACAAAGA ACATCCCGAA 720
CCCAAGATTG AGAGGATGGG TGATAGTTT GCTGTGAAA TCAAGGGTAG AATCCACTTT 780
GATCTTTTCC CAGTTGTGCG AAGGACGATA AACCTCCCAA CGTATACGCT TGAGGCAAGT 840

Replacement Figure


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TATGAAGCAG TTTTAGGAAA AACCAAAAGC AAATTAGGAG CAGAGGAAAT TGCCGCTATA 900
TGGGAAACAG AAGAAAGCAT GAAAAAATA GCCCAGTACT CAATGGAAGA TGCTAGGGCA 960
ACGTATGAGC TCGGGAAGGA ATTCTTCCCC ATGGAAGCTG AGCTGGCAAA GCTGATAGGT 1020
CAAAGTGAT GGGACGTCTC GAGATCAAGC ACCGGCAACC TCGTGGAGTG GTATCTTTTA 1080
AGGGTGGCAT ACGCGAGGAA TGAAC TTGCA CCGAACAAAC CTGATGAGGA AGAGTATAAA 1140
CGGCGCTTAA GAACAACCTTA CCTGGGAGGA TATGTAAAAG AGCCAGAAAA AGGTTTGTGG 1200
GAAAATATCA TTTATTTGGA TTTCCGCAGT CTGTACCCCT CAATAATAGT TACTCACAA 1260
GTATCCCCAG ATACCCTTGA AAAAGAGGGC TGTAAGAAAT ACGATGTTGC TCCGATAGTA 1320
GGATATAGGT TCTGCAAGGA CTTTCCGGGC TTTATTCCCT CCATACTCGG GGACTTAATT 1380
GCAATGAGGC AAGATATAAA GAAGAAAAATG AAATCCACAA TTGACCCGAT CGAAAAAGAAA 1440
ATGCTCGATT ATAGGCAAG AGCTATTAAA TTGCTTGCAA ACAGCTATTA CGGCTATATG 1500
GGGTATCCTA AGGCAAGATG GTACTCGAAG GAATGTGCTG AAAGCGTTAC CGCATGGGG 1560
AGACACTACA TAGAGATGAC GATAAGAGAA ATAGAGGAAA AGTTCCGGCTT TAAGGTTCTT 1620
TATGCGGACA CTGACGGCTT TTATGCCACA ATACCCGGGG AAAAGCCTGA ACTCATTA 1680
AAGAAAGCCA AGGAATTCCT AACTACATA AACTCCAAC TTCCAGGTCT GCTTGAGCTT 1740
GAGTATGAGG GCTTTTACTT GAGAGGATTC TTGTGTACAA AAAAGCGCTA TGCAGTCATA 1800
GATGAAGAGG GCAGGATAAC AACAAAGGGC TTGGAAGTAG TAAGGAGAGA TTGGAGTGAG 1860
ATAGCTAAGG AGACTCAGGC AAAGGTTTTA GAGGCTATAC TTAAAGAGGG AAGTGTGAA 1920
AAAGCTGTAG AAGTTGTTAG AGATGTTGTA GAGAAAATAG CAAAATACAG GGTCCACTT 1980
GAAAAGCTTG TTATCCATGA GCAGATTACC AGGATTTAA AGGACTACAA AGCCATTGGC 2040
CCTCATGTCC CGATAGCAAA AAGACTTGCC GCAAGAGGGA TAAAAGTGAA ACCGGGCACA 2100
ATAATAAGCT ATATCGTTCT CAAAGGGAGC GGAAGATAA GCGATAGGGT AATTTACTT 2160
ACAGAAATACG ATCCTAGAAA ACACAAGTAC GATCCGGACT ACTACATAGA AAACCAAGTT 2220
TTGCCGGCAG TACTTAGGAT ACTCGAAGCG TTGCGATACA GAAAGGAGGA TTTAAGGTAT 2280
CAAAGCTCAA AACAAACCGG CTTAGATGCA TGGCTCAAGA GG 2325 //
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// GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG
   ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
   GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
   CTG CAG ATG CTG GAG AAG CAG AAA AAG // TGA
```

Figure 17000

Deep Vent- Ssod7 DNA polymerase fusion protein

Nucleotide sequence (SEQ ID NO: 37) // Nucleotide sequence (SEQ ID NO: 71)
Nucleotide sequence (SEQ ID NO: 38) // Nucleotide sequence (SEQ ID NO: 71)

Replacement Figure

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATACTTG	ACGCTGACTA	CATCACCGAG	GATGGGAAGC	CGATTATAAG	GATTTTCAAG	60
AAAGAAAACG	GCGAGTTTAA	GTTTGAGTAC	GACAGAAACT	TTAGACCCTTA	CATTTACGCT	120
CTCCTCAAAG	ATGACTCGCA	GATTGATGAG	GTTAGGAAGA	TAACCGCCGA	GAGCAATGGG	180
AAGATAGTGA	GAATTATAGA	TGCCGAAAAG	GTAAGGAAGA	AGTTCCTGGG	GAGGCCGATT	240
GAGGTATGGA	GGCTGTACTT	TGAACACCCT	CAGGACXXXC	CCGCAATAAG	GGATAAGATA	300
AGAGAGCATT	CCGCAGTTAT	TGACATCTTT	GAGTACGACA	TTCCGTTTCG	GAAGAGGTAC	360
CTAATAGACA	AAGGCCCTAAT	TCCAATGGAA	GGCGATGAAG	AGCTCAAGTT	GCTCGCATTT	420
GACATAGAAA	CCCTCTATCA	CGAAGGGGAG	GAGTTCGCGA	AGGGCCCCAT	TATAATGATA	480
AGCTATGCTG	ATGAGGAAGA	AGCCAAAGTC	ATAACGTGGA	AAAAGATCGA	TCTCCCCTAC	540
GTCGAGGTAG	TTTCCAGCGA	GAGGGAGATG	ATAAAGCGGT	TCCTCAAGGT	GATAAGGGAG	600
AAAGATCCCC	ATGTTATAAT	TACCTACAAC	GGCGATTCTT	TCGACCTTCC	CTATCTAGTT	660
AAGAGGGCCG	AAAAGCTCGG	GATAAAGCTA	CCCTTGGGAA	GGACGGTAG	TGAGCCAAAAG	720
ATGCAGAGGC	TTGGGGATAT	GACAGCGGTG	GAGATAAAGG	GAAGGATACA	CTTTGACCTC	780
TACCACGTGA	TTAGGAGAAC	GATAAACCTC	CCAACATACA	CCCTCGAGGC	AGTTTATGAG	840
GCAATCTTCG	GAAAGCCAAA	GGAGAAAAGTT	TACGCTCAGG	AGATAGCTGA	GGCCTGGGAG	900
ACTGGAAAGG	GACTGGAGAG	AGTTGCAAAG	TATTCAATGG	AGGATGCAAA	GGTAACGTAC	960
GAGCTCGGTA	GGGAGTTCTT	CCCAATGGAG	GCCCAGCTTT	CAAGGTTAGT	CGGCCAGCCC	1020
CTGTGGGATG	TTTCTAGGTC	TTCAACTGGC	AACCTGGTGG	AGTGGTACCT	CCTCAGGAAAG	1080
GCCTACGAGA	GGAATGAATT	GGCTCCAAAC	AAGCCGGATG	AGAGGGAGTA	CGAGAGAAGG	1140
CTAAGGGAGA	GCTACGCTGG	GGGATACGTT	AAGGAGCCGG	AGAAAAGGGG	CTGGGAGGGG	1200
TTAGTTTCCC	TAGATTTTCAG	GAGCCTGTAC	CCCTCGATAA	TAATCACCCA	TAACGTCCTCA	1260
CCGGATACGC	TGAACAGGGA	AGGGTGTAGG	GAATACGATG	TCGCCCCAGA	GGTTGGGCAC	1320
AAGTTCTGCA	AGGACTTCCC	GGGGTTTATC	CCCAGCCTGC	TCAAGAGGTT	ATTGGATGAA	1380
AGGCAAGAAA	TAAAAAGGAA	GATGAAAAGCT	TCTAAAGACC	CAATCGAGAA	GAAGATGCTT	1440
GATTACAGGC	AACGGGCAAT	CAAAATCCTG	GCAAACAGCT	ATTATGGGTA	TTATGGGTAC	1500
GCAAAAAGCCC	GTTGGTACTG	TAAGGAGTGC	GCAGAGAGCG	TTACGGCCTG	GGGAGGGAA	1560
TATATAGAGT	TCGTAAAGGA	GAAACTGGAG	GAAAAGTTTCG	GGTTCAAAAGT	CTTATACATA	1620
GACACAGATG	GACTCTACGC	CACAATTCTT	GGGGCAAAAC	CCGAGGAGAT	AAAGAAGAAA	1680
GCCCTAGAGT	TCGTAGATTA	TATAAACGCC	AAGCTCCCAG	GGCTGTTGGA	GCTTGAGTAC	1740
GAGGGCTTCT	ACGTGAGAGG	GTTCTTTCGTG	ACGAAGAAGA	AGTATGCGTT	GATAGATGAG	1800
GAAGGGAAGA	TAATCACTAG	GGGGCTTGAA	ATAGTCAGGA	GGGACTGGAG	CGAAATAGCC	1860
AAAGAAACCC	AAGCAAAAGT	CCTAGAGGCT	ATCCTAAAGC	ATGGCAACGT	TGAGGAGGCA	1920
GTAAGAGATAG	TTAAGGAGGT	AAC TGAAAAG	CTGAGCAAGT	ACGAAATACC	TCCAGAAAAG	1980
CTAGTTATTT	ACGAGCAGAT	CACGAGGCC	CTTCACGAGT	ACAAGGCTAT	AGGTCCGCAC	2040
GTTGCCGTGG	CAAAAAGGTT	AGCCGCTAGA	GGAGTAAAGG	TGAGGCCTGG	CATGGTGATA	2100
GGGTACATAG	TGCTGAGGGG	AGACGGGCCA	ATAAGCAAGA	GGCTATCCT	TGCAGAGGAG	2160
TTCGATCTCA	GGAAGCATAA	GTATGACGCT	GAGTATTACA	TAGAAAATCA	GGTTTACCT	2220
GCCGTTCTTA	GAATATTAGA	GGCCTTTGGG	TACAGGAAAG	AAGACCTCAG	GTGGCAGAAG	2280
ACTAAACAGA	CAGGTCTTAC	GGCATGGCTT	AACATCAAGA	AGAAG		2328

Replacement Figure

```
// GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA GAG GTA GAC ATC TCC AAG
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
CTG CAG ATG CTG GAG AAG CAG AAA AAG // TGA
```

Figure 17PPP

Ssod7 - Deep Vent DNA polymerase fusion protein

Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 37)

Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 38)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```
//GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAG GAG GTA GAC ATC TCC AAG
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
CTG CAG ATG CTG GAG AAG CAG AAA AAG //
```

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ATGATACTTG ACGTGACTA CATCACCAG GATGGGAAGC CGATTATAAG GATTTCAAG 60
AAAGAAACG GCGAGTTTAA GGTGAGTAC GACAGAAACT TTAGACCTTA CATTTACGCT 120
CTCCTCAAAG ATGACTCGCA GATTGATGAG GTTAGGAAGA TAACCGCCGA GAGCATGGG 180
AAGATAGTGA GAATTATAGA TGCCGAAAG GTAAGGAAGA AGTTCCTGG GAGCCGATT 240
GAGGTATGGA GGCTGTACTT TGAACACCCT CAGGACXXXC CCGCAATAAG GGATAAGATA 300
AGAGAGCATT CCGCAGTTAT TGACATCTTT GAGTACGACA TTCCGTTTCG GAAGAGGTAC 360
CTAATAGACA AAGGCCTAAT TCCAATGGAA GCGATGAAG AGCTCAAGTT GCTCGCATTT 420
GACATAGAAA CCTCTATCA CGAAGGGGAG GAGTTCGCGA AGGGCCCAT TATAATGATA 480
AGCTATGCTG ATGAGGAAGA AGCCAAAGTC ATAACGTGGA AAAAGATCGA TCTCCCGTAC 540
GTCGAGGTAG TTTCCAGCGA GAGGAGATG ATAAAGCGGT TCCTCAAGGT GATAAGGGAG 600
AAAGATCCCG ATGTTATAAT TACCTACAAC GCGGATTCTT TCGACCTTCC CTATCTAGTT 660
AAGAGGGCCG AAAAGCTCGG GATAAAGCTA CCCCTGGGAA GGGACGGTAG TGAGCCAAAG 720
ATGCAGAGGC TTGGGGATAT GACAGCGGTG GAGATAAAGG GAAGGATACA CTTTGACCTC 780
```

Replacement Figure

TACCACGTGA	TTAGGAGAAC	GATAAACCTC	CCAACATACA	CCCTCGAGGC	AGTTTATGAG	840
GCAATCTTCG	GAAAGCCAAA	GGAGAAAGTT	TACGCTCACG	AGATAGCTGA	GGCCTGGGAG	900
ACTGGAAAGG	GACTGGAGAG	AGTTGCAAAG	TATTCAATGG	AGGATGCAAA	GGTAACGTAC	960
GAGCTCGGTA	GGGAGTTCTT	CCCAATGGAG	GCCCAGCTTT	CAAGGTTAGT	CGGCCAGCCC	1020
CTGTGGGATG	TTTCTAGGTC	TTCAACTGGC	AAC TTGGTGG	AGTGGTACCT	CCTCAGGAAG	1080
GCCTACGAGA	GGAATGAATT	GGCTCCA AAC	AAGCCGGATG	AGAGGGAGTA	CGAGAGAAGG	1140
CTAAGGGAGA	GCTACGCTGG	GGGATACGTT	AAGGAGCCGG	AGAAAAGGCT	CTGGGAGGGG	1200
TTAGTTTCCC	TAGATTTCAG	GAGCCTGTAC	CCCTCGATAA	TAATCACCCA	TAACGTCCTA	1260
CCGGATACGC	TGAACAGGGA	AGGGTG TAGG	GAATACGATG	TCGCCCCAGA	GGTTGGGCAC	1320
AAGTTCTGCA	AGGACTTCCC	GGGGTTTATC	CCCAGCCTGC	TCAAGAGGTT	ATTGGATGAA	1380
AGGCAAGAAA	TAAAAGGAA	GATGAAAAGCT	TCTAAAGACC	CAATCGAGAA	GAAGATGCTT	1440
GATTACAGGC	AACGGGCAAT	CAAAATCCTG	GCAAACAGCT	ATTATGGGTA	TTATGGGTAC	1500
GCAAAAGCCC	GTTGGTACTG	TAAGGAGTGC	GCAGAGAGCG	TTACGGCCTG	GGGAGGGGAA	1560
TATATAGAGT	TCGTAAGGAA	GGA ACTGGAG	GAAAAGTTTCG	GGTTCAAAAGT	CTTATACATA	1620
GACACAGATG	GACTCTACGC	CACAATTCTT	GGGGCAAAAC	CCGAGGAGAT	AAAGAAAGAAA	1680
GCCCTAGAGT	TCGTAGATTA	TATAAACGCC	AAGCTCCCAG	GGCTGTTGGA	GCTTGAGTAC	1740
GAGGGCTTCT	ACGTGAGAGG	GTTCTTTCGTG	ACGAAAGAAGA	AGTATGCGTT	GATAGATGAG	1800
GAAGGGAAGA	TAATCACTAG	GGGGCTTGAA	ATAGTCAGGA	GGGACTGGAG	CGAAATAGCC	1860
AAAGAAACCC	AAGCAAAAGT	CCTAGAGGCT	ATCCTAAAGC	ATGGCAACGT	TGAGGAGGCA	1920
GTAAAGATAG	TTAAGGAGGT	AACTGAAAAG	CTGAGCAAGT	ACGAAATACC	TCCAGAAAAAG	1980
CTAGTTATTT	ACGAGCAGAT	CACGAGGCC	CTTCACGAGT	ACAAGGCTAT	AGGTCCGCAC	2040
GTTGCCGTGG	CAAAAAGGTT	AGCCGCTAGA	GGAGTAAAGG	TGAGGCCCTGG	CATGGTGATA	2100
GGGTACATAG	TGCTGAGGGG	AGACGGGCCA	ATAAGCAAGA	GGGCTATCCT	TGCAGAGGAG	2160
TTCGATCTCA	GGAAGCATAA	GTATGACGCT	GAGTATTACA	TAGAAAATCA	GGTTTTCACCT	2220
GCCGTTCTTA	GAATATTAGA	GGCCTTTGGG	TACAGGAAAG	AAGACCTCAG	GTGGCAGAAG	2280
ACTAAACAGA	CAGGTCTTAC	GGCATGGCTT	AACATCAAGA	AGAAG TAA		2328

Figure 17QQQ

JDF-3 - Sso7d fusion protein

Nucleotide sequence (SEQ ID NO: 39) // Nucleotide sequence (SEQ ID NO: 71)

Nucleotide sequence (SEQ ID NO: 40) // Nucleotide sequence (SEQ ID NO: 71)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATCCTTGACGTTGATTACATCACCGAGAATGGAAGCCCGTCATCAGGGTCTTCAAGAAGGAGAACGGCGAGTTCAGGATTGAATACGACCGGAGTTCGAGCCCTACTTCT
ACGCGCTCCTCAGGGACGACTCTGCCATCGAAGAAATCAAAAAGATAACCGCGGAGAGCGACGGCGTGGTTAAGGTTAAGCGCGGAGAGGTTGAAGAAAAAGTTCCCTCGG
CAGGTCTGTGGAGGTCTGGGTCTCTACTTCAACGCCACCCCGCAGGACXXXCCCGGCAATCCGCGACAAAAATAAGGAAGCACCCCGGTCATCGACATCTACGAGTACGACATACCC

Replacement Figure

TTCCGCCAAGCGCTACCTCATAGACAAGGGCCCTAATCCCGATGGAAAGGTGAGGAAGAGCTTAAACTCAIGTCCTTCCGACATCGAGCGCTCTACCCAGGAGGAGAAAGAGTTTGGAA
CCGGGCCGATTCTGTATGATAAGCTACGCCGATGAAAGCGAGGCGCGGTGATAACCTGGAAGAAGATCGACCTTCTTACGTTGAGGTTGTCTCCACCGAGAAGGAGATGATTAA
GCGCTTCTTGAGGTCGTTAAGGAGAAAGGACCCGGACGTCGTGATAACATACAACGGGACAACTTCGACTTCGCCTACCTGAAAAGCGCTGTGAGAAAGCTTGGCGTGAGCTTT
ACCTTCGGGAGGACGGGAGCGGAGCCGAAGATACAGCGCATGGGGACAGGTTTTCGGTCGAGGTGAAGGCAGGTACACTTCGACCTTTATCCAGTCATAAGGCCGACCATAA
ACCTCCCGACCTACACCCCTTGAGGCTGTATACGAGCGGTTTTCGGCAAGCCCAAGGAGAGGTCTACGCCGAGGAGATAGCCACCGCTGGGAGACCGGCGAGGGCTTGAGAG
GGTCGGCGCTACTCGATGGAGGACGCGAGGGTTACCTACGAGCTTGGCAGGGAGTTCTTCCCGATGGAGGCCAGCTTTCAGGCTCATCGGCCAAGCCCTCTGGGACGTTTCC
CGCTCCAGCACCGGCAACCTCGTCGAGTGGTTCCCTAAGGAAGCCCTACGAGAGGAACGAACTCGCTCCCAACAAGCCGACGAGAGGAGCTGGCGAGGAGAAGGGGGGCT
ACGCGGTGGCTACGTCAAGGAGCCGGAGCGGGGACTGTGGGACAATATCGTGATCTAGACTTTTCGTAGTCTCTACCCCTTCAATCATATAATCACCCACAACGTCCTCGCCAGATAC
GCTCAACCCGAGGGGTAGGAGCTACGACGTTGCCCGGAGGTCACAAAGTTCTGCAAGGACTTCCCGGCTTCATTCGAGCCTGCTCGGAAACCTGCTGGAGGAAGG
CAGAAGATAAAGAGGAAGATGAAGGCAACTCTCGACCCGCTGGAGAAGAATCTCCTCGATTACAGGCAACGCGCATCAAGATTCTCGCCAAACAGTACTACGGCTACTACGGCT
ATGCCAGGGCAAGATGGTACTCGAGGGAGTGCCCGAGAGCGTTACGGCATGGGGAAGGAGTACATCGAAATGGTCAATCAGAGAGCTTGAGGAAAAGTTTCGGTTTAAAGTCCT
CTATGCAGACACAGCGGTCCTCATGCCCACCATTCCTTGAGCGGACGCTGAAACAGTCAAGAAAAGGCAATGGAGTTCTTAAACTATATCAATCCCAAACTGCCCGCCTTCTC
GAACTCGAATACGAGGGCTTCTACGTACGAGGGCTTCTTCGTACGAAAGAAAAGTACGCGGTCAATCGACGAGGAGGCAAGATAACCAACGCGGGGCTTGAGATAGTCAGGGCGG
ACTGGAGCGAGATAGCGAAGGAGACGCGAGCGAGGGTTTGGAGCGGATACTCAGGCACGGTGACGTTGAAGAGGCCGTCAGAAATTGTCAGGGAAGTCACCGAAAAGCTGAGCAA
GTACGAGGTTCCGCCGGAGAAAGCTGGTTATCCACGAGCAGATAACGCGCGAGCTCAAGGACTACAAGCCCGGACCGGCGATAGCCATAGCCGAAGCGTTTGGCCCGCCAGAGGT
GTTAAATCCGGCCCCGAACTGTGATAAGCTACATCGTTCTGAAGGCTCCGGAAGGATAGGCGACAGGGCGATTCCCTTCGACGAGTTCGACCCGACGAAACACAAGTACGATG
CGGACTACTACATCGAGAACCAAGGTTCTGCGGCGAGTTGAGAGAAATCCTCAGGGCTTTCGGCTACCGCAAGGAAGACCTGCGCTACCAGAAAGACGAGGACGAGTCTGGGCTTGGCGC
GTGGCTGAAGCCGAAGGGGAAGAAAG//

//GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA GAG GTA GAC ATC TCC AAG
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
CTG CAG ATG CTG GAG AAG CAG AAA AAG // TAG

Figure 17RRR

Sso7d - JDF-3 fusion protein

Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 39)

Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 40)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

//GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA GAG GTA GAC ATC TCC AAG
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
CTG CAG ATG CTG GAG AAG CAG AAA AAG //

Replacement Figure

ATGATCCTTGACGTTGATTACATCACCGAGAAATGGAAAGCCCGTCAATCAGGGTCTTCAAGAAAGGAGAACGGCGAGTTTGAATACGACCGCGAGTTTCGAGCCCTACTTCT
ACGCGCTCCTCAGGGACGACTCTGCCATCGAAGAAATCAAAAAGATAAACCGCGAGAGGCACGGTCGTTAAGGTTAAGCGCGGAGAGGTGAAGAAAAGTTCCCTCGG
CAGGTCGTGGAGGTCGTGGTCCCTACTTACGCAACCGCAGGACXXXCCGGCAATCCGCGACAAAATAAGGAAGCACCCCGGTCATCGACATCTACGAGTACGACATACCC
TTCGCCAAGCGCTACCTCATAGACAAGGGCCTAATCCCCGATGGAAAGGTGAGGAAGCTTAAACTCATGTCTTCGACATCGAGACGCTCTACCACGAGGGAAGAGTTTGGAA
CCGGCCGATTCTGATGATAAGCTACGCCGATGAAGCGAGCGCGTGATAACCTGGAAGAAGATCGACCTTCCCTTACGTTGAGGTTGTCTCCACCGAGAAGGAGATGATTAA
GCGCTTCTTGAGGTCGTTAAGGAGAAAGGACCCGGACGTGCTGATAACATACAGCGCACAACTTCGACTTCGCCCTACCTGAAAAGCGCTGTGAGAAAGCTTGGCGTGAGCTTT
ACCTCGGGAGGACGGGAGCGAGCCGAAGATACAGCGCATGGGGACAGGTTTTCGGTCGAGGTGAAGGCGAGGTACACTTCGACCTTTATCCAGTCATAAGGCGCACCATAA
ACCTCCCGACCTACACCTTGAGGCTGTATACGAGGCGGTTTTCGGCAAGCCCAAGGAGAAAGTCTACGCCGAGGAGATAGCCACCGCTGGGAGACCGGGCGAGGGCTTGGAGAG
GGTCGCGCGCTACTCGATGGAGGACCGGAGGTTACCTACGAGCTTGGCAGGAGTTCTTCCCGATGGAGGCCAGCTTTCAGGCTCATCGGCCAAGGCTCTGGGACGTTTCC
CGTCCAGCACCGGCAACCTCGTCGAGTGGTTCCCTAAGGAAGGCTACGAGAGGAACGAACTCGCTCCAAAGCCGACGAGAGGAGCTGGCGGAGGAGAAAGGGGGGCT
ACGCGGTGGCTACGTCAAGGAGCCGGAGCGGGGACTGTGGGACAAATATCGTGATCTAGACTTTCGTAGTCTTAQCCCTTCAATCATAATCACCCACAACGCTCTGCCAGATAC
GCTCAACCGCGAGGGGTAGGAGCTACGACGTTGCCCGAGGTCGGTCACAAGTTCTGCAAGGACTTCCCGGCTTCATTCGAGCCTGCTCGGAAACCTGCTGGAGGAAAGG
CAGAAGATAAAGAGGAAGATGAAGCAACTCTCGACCCGCTGGAGAAAGAAATCTCCTCGATTACAGGCAACGGCGCATCAAGATTCTCGCCAAACAGCTACTACGGCTACACGGCT
ATGCCAGGGCAAGATGGTACTGCAAGGAGTCCGCCGAGAGCGGTTACGGCATGGGGAAGGGAGTACATCGAAATGGTCAATCAGAGAGCTTGAGGAAAAGTTCCGTTTAAAGTCCT
CTATGCAGACACAGACGGTCTCCATGCCACCATTCCTGGAGCGGACGCTGAACAGTCAAGAAAAGCAATGGAGTTCTTAAACTATATCAATCCCAACCTGCCCCCTTCTC
GAACTCGAATACGAGGGCTTCTACGTCAAGGGCTTCTTCGTCAACGAAGAAAAGTACGCGGTCAACGAGGAGGCAAGATAACACCGCGGGCTTGAGATAGTCAGGCGCG
ACTGGAGCGAGATAGCGAAGGAGACGAGCGAGGGTTTGGAGGCGATACTCAGGCACGGTGACGTTGAAGAGGCCGTAGAAATTGTCAGGGAAGTCAACGAAAAGCTGAGCAA
GTACGAGGTTCCGCCGGAGAACTGGTTATCCACGAGCAGATAACGCGCGAGCTCAAGGACTACAAGGCCACCGGCCCGCAGTAGCCATAGCGAAGCGTTTGGCCCGCCAGAGGT
GTTAAAATCCGGCCCGGAACGTGTGATAAGCTACATCGTTCTGAAGGGCTCCGGAAGGATAGGCGACAGGGCGATTCCCTTCGACGAGTTTCGACCCGACGAAAGCACAAAGTACGATG
CGGACTACTACATCGAGAACCAAGGTTCTGCCGGCAGTTGAGAGAAATCCTCAGGGCCCTTCGGCTACCCGCAAGGAAGACCTGCGCTACCAGAAGACGAGGCAGGTCGGGCTTGGCGC
GTGGCTGAAGCCGAAGGGGAAGAGTGA

MkTpV 1 valvydaefvgserfeeeeetflkgvkaYdgvdvRVLmERSSbaKudeEllaElhq
ReCA VI GdnAlkiyaBVRudLrIbaPKdgdEvvg

MkTpV 179 vPIDskILILwtpbEARGLSVSevggkdpessgiyslwsrvvvn
HTH asnC IDiILILeLRRISEARGLSVStvevr

HTH SS HTH α

	299	354	411	468	518	568	622	696	752	803	855	912	73	57	93	Consensus				
A	l	a	a	a	l	i	k	w	y	l	e	k	k	a	e	l				
B	t	d	k	k	s	r	e	s	d	n	r	v	d	k	k	p	u			
C	d	e	k	k	s	r	e	s	d	n	r	v	d	k	k	p	u			
D	r	e	r	r	e	r	e	r	e	r	e	r	e	r	e	r	g			
E	r	e	r	r	e	r	e	r	e	r	e	r	e	r	e	r	g			
F	r	e	r	r	e	r	e	r	e	r	e	r	e	r	e	r	g			
G	r	e	r	r	e	r	e	r	e	r	e	r	e	r	e	r	g			
H	r	e	r	r	e	r	e	r	e	r	e	r	e	r	e	r	g			
I	r	e	r	r	e	r	e	r	e	r	e	r	e	r	e	r	g			
J	r	e	r	r	e	r	e	r	e	r	e	r	e	r	e	r	g			
K	r	e	r	r	e	r	e	r	e	r	e	r	e	r	e	r	g			
L	r	e	r	r	e	r	e	r	e	r	e	r	e	r	e	r	g			
EcRuV	r	e	r	r	e	r	e	r	e	r	e	r	e	r	e	r	g			
HsPol	r	e	r	r	e	r	e	r	e	r	e	r	e	r	e	r	g			
TaqPol	r	e	r	r	e	r	e	r	e	r	e	r	e	r	e	r	g			
Consensus	r	e	r	r	e	r	e	r	e	r	e	r	e	r	e	r	g			
HhH	r	e	r	r	e	r	e	r	e	r	e	r	e	r	e	r	g			
SS	r	e	r	r	e	r	e	r	e	r	e	r	e	r	e	r	g			

Replacement Figure

FIGURE 19

SEQ ID NO: 120 Synthetic Sso7d gene

GCAACCGTAAAGTTCAAGTACAAAGGCGAAGAAAAAGAGGTAGACATCTCCAA
GATCAAGAAAGTATGGCGTGTGGGCAAGATGATCTCCTTCACCTACGACGAGGG
CGGTGGCAAGACCGGCCGTGGTGCGGTAAGCGAAAAGGACGCGCCGAAGGAGC
TGCTGCAGATGCTGGAGAAG CAGAAAAAG

SEQ ID NO: 121 The amino acid sequence of Sso7d.

ATVKFKYKGEEKEVDISKIKKVWRVGKMISFTYDEGGGKTGRGAVSEKDAPKELLQ
MLEKQKK

SEQ ID NO: 122 The DNA sequence encoding the Sso7d-ΔTaq fusion protein

ATGATTACGAATTCGAGCGCAACCGTAAAGTTCAAGTACAAAGGCGAAGAAAAA
GAGGTAGACATCTCCAAGATCAAGAAAGTATGGCGTGTGGGCAAGATGATCTCC
TTCACCTACGACGAGGGCGGTGGCAAGACCGGCCGTGGTGCGGTAAGCGAAAAG
GACGCGCCGAAGGAGCTGCTGCAGATGCTGGAGAAGCAGAAAAAGGGCGGCGG
TGTCAGTAGTCCCAAGGCCTGGAGGAGGCCCCCTGGCCCCCGCCGGAAGGGGCC
TTCGTGGGCTTTGTGCTTTCCCGCAAGGAGCCCATGTGGGCCGATCTTCTGGCCCT
GGCCGCCGCCAGGGGGGGCGGGTCCACCGGGCCCCCGAGCCTTATAAAGCCCT
CAGGGACCTGAAGGAGGCGCGGGGGCTTCTCGCCAAAGACCTGAGCGTTCTGGC
CCTGAGGGAAGGCCTTGGCCTCCCGCCCCGGCGACGACCCCATGCTCCTCGCCTAC
CTCCTGGACCCTTCCAACACCACCCCCGAGGGGGTGGCCCCGGCGCTACGGCGGG
GAGTGGACGGAGGAGGCGGGGGAGCGGGCCGCCCTTCCGAGAGGCTCTTCGCC
AACCTGTGGGGGAGGCTTGAGGGGGAGGAGAGGCTCCTTTGGCTTTACCGGGAG
GTGGAGAGGCCCCCTTCCGCTGTCCTGGCCACATGGAGGCCACGGGGGTGCGC
CTGGACGTGGCCTATCTCAGGGCCTTGTCCCTGGAGGTGGCCGAGGAGATCGCCC
GCCTCGAGGCCGAGGTCTTCCGCCTGGCCGGCCACCCCTTCAACCTCAACTCCCG
GGACCAGCTGGAAAGGGTCCTCTTTGACGAGCTAGGGCTTCCCGCCATCGGCAA
GACGGAGAAGACCGGCAAGCGCTCCACCAGCGCCGCGCTCCTGGAGGCCCTCCG
CGAGGCCACCCCATCGTGGAGAAGATCCTGCAGTACCGGGAGCTCACCAAGCT
GAAGAGCACCTACATTGACCCCTTGCCGGACCTCATCCACCCAGGACGGGCGG
CCTCCACACCCGCTTCAACCAGACGGCCACGGCCACGGGCAGGCTAAGTAGCTC
CGATCCCAACCTCCAGAACATCCCCGTCCGCACCCCGCTTGGGCAGAGGATCCGC
CGGGCCTTCATCGCCGAGGAGGGGTGGCTATTGGTGGCCCTGGACTATAGCCAG
ATAGAGCTCAGGGTGCTGGCCACCTCTCCGGCGACGAGAACCTGATCCGGGTCT
TCCAGGAGGGGGCGGGACATCCACACGGAGACCGCCAGCTGGATGTTTCGGCGTCC
CCCGGGAGGCCGTGGACCCCTGATGCGCCGGGCGGCCAAGACCATCAACTTCG
GGGTCCTCTACGGCATGTGCGGCCACCGCCTCTCCAGGAGCTAGCCATCCCTTA
CGAGGAGGCCAGGCCTTCAATTGAGCGCTACTTTAGAGCTTCCCCAAGGTGCGG
GCCTGGATTGAGAAGACCCTGGAGGAGGGCAGGAGGCGGGGGTACGTGGAGAC
CCTCTTCGGCCGCCGCGCTACGTGCCAGACCTAGAGGCCCGGGTGAAGAGCGT
GCGGGAGGCGGCCGAGCGCATGGCCTTCAACATGCCCGTCCAGGGCACCGCCGC
CGACCTCATGAAGCTGGCTATGGTGAAGCTCTTCCCCAGGCTGGAGGAAATGGG
GGCCAGGATGCTCCTTCAGGTCCACGACGAGCTGGTCCTCGAGGCCCAAAAGA
GAGGGCGGAGGCCGTGGCCCGGCTGGCCAAGGAGGTCATGGAGGGGGTGTATCC
CCTGGCCGTGCCCTGGAGGTGGAGGTGGGGATAGGGGAGGACTGGCTCTCCGC
CAAGGAGGGCATTGATGGCCGCGGCGGAGGCGGGCATCATCATCATCATTAA

SEQ ID NO: 123 The amino acid sequence of Sso7d-ΔTaq fusion protein

MITNSSATVKFKYKGEEKEVDISKIKKVWRVGKMISFTYDEGGGKTGRGAVSEKDA
PKELLQMLEKQKKGGGVTSKALEEAPWPPPEGAFVGVLSRKEPMWADLLALAA

ARGGRVHRAPEPYKALRDLKEARGLLAKDLSVLALREGLGLPPGDDPMLLAYLLDP
SNTTPEGVARRYGGEWTEEAGERAAALSERLFANLWGRLEGEERLLWLYREVERPLS
AVLAHMEATGVRLDVAYLRALSLEVAEEIARLEAEVFRLAGHPFNLNSRDQLERVLF
DELGLPAIGKTEKTGKRSTSAAVLEALREAHPIVEKILQYRELTKLKSTYIDPLPDLIH
PRTGRLHTRFNQTATATGRLSSSDPNLQNIPVRTPLGQRIRRAFIAEEGWLLVALDYS
QIELRVLAHLSGDENLIRVFQEGRDIHTETASWMFGVPREAVDPLMRRAAKTINFGV
LYGMSAHRLSQELAIPYEEAQAFIERYFQSFVKVRAWIEKTLEEGRRRGYVETLFGRR
RYVPDLEARVKSUREAAERMAFNPVQGTAAADLMKCLAMVKLFPRLEEMGARMMLL
QVHDELVLAPKERAEEAVARLAKEVMIEGVYPLAVPLEVEVGIGEDWLSAKEGIDGR
GGGGHHHHHH

SEQ ID NO: 124 The DNA sequence encoding the Sso7d-Taq fusion protein

ATGATTACGAATTCGAGCGCAACCGTAAAGTTCAAGTACAAAGGCGAAGAAAAA
GAGGTAGACATCTCCAAGATCAAGAAAGTATGGCGTGTGGGCAAGATGATCTCC
TTCACCTACGACGAGGGCGGTGGCAAGACCGGCCGTGGTGCGGTAAGCGAAAAG
GACGCGCCGAAGGAGCTGCTGCAGATGCTGGAGAAGCAGAAAAAGGGCGGGCGG
TGTCAGTAGTGGGATGCTGCCCCCTCTTTGAGCCCAAGGGCCGGGTCTCCTGGTG
GACGGCCACCACCTGGCCTACCGCACCTTCCACGCCCTGAAGGGCCTCACCACCA
GCCGGGGGGAGCCGGTGCAGGCGGTCTACGGCTTCGCCAAGAGCCTCCTCAAGG
CCCTCAAGGAGGACGGGGACGCGGTGATCGTGGTCTTTGACGCCAAGGCCCCCT
CCTTCCGCCACGAGGCCTACGGGGGGGTACAAGGCGGGGCCGGGCCCCCACGCCAG
AGGACTTTCCCCGGCAACTCGCCCTCATCAAGGAGCTGGTGACCTCCTGGGGCT
GGCGCGCCTCGAGGTCCCGGGCTACGAGGCGGACGACGTCCTGGCCAGCCTGGC
CAAGAAGGCGGAAAAGGAGGGCTACGAGGTCCGCATCCTCACCGCCGACAAAG
ACCTTTACCAGCTCCTTTCCGACCGCATCCACGTCCTCCACCCCGAGGGGTACCT
CATCACCCCGGCCTGGCTTTGGGAAAAGTACGGCCTGAGGCCCGACCAGTGGGC
CGACTACCGGGCCCTGACCGGGGACGAGTCCGACAACCTTCCCGGGGTCAAGGG
CATCGGGGAGAAGACGGCGAGGAAGCTTCTGGAGGAGTGGGGGAGCCTGGAAG
CCCTCCTCAAGAACCTGGACCGGCTGAAGCCCGCCATCCGGGAGAAGATCCTGG
CCCACATGGACGATCTGAAGCTCTCCTGGGACCTGGCCAAGGTGCGCACCGACCT
GCCCCTGGAGGTGGACTTCGCCAAAAGGCGGGAGCCCCGACCGGGAGAGGCTTAG
GGCCTTTCTGGAGAGGCTTGAGTTTGGCAGCCTCCTCCACGAGTTCGGCCTTCTG
GAAAGCCCCAAGGCCTGGAGGAGGCCCCCTGGCCCCCGCCGGAAGGGGCCTTC
GTGGGCTTTGTGCTTTCCCGCAAGGAGCCCATGTGGGGCCGATCTTCTGGCCCTGG
CCGCCGCCAGGGGGGGCGGGTCCACCGGGCCCCCGAGCCTTATAAAGCCCTCA
GGGACCTGAAGGAGGCGCGGGGGCTTCTCGCCAAAGACCTGAGCGTTCTGGCCC
TGAGGGAAGGCCTTGGCCTCCCGCCCGGCGACGACCCCATGCTCCTCGCCTACCT
CCTGGACCCTTCCAACACCACCCCGAGGGGGTGGCCCGGCGCTACGGCGGGGA
GTGGACGGAGGAGGCGGGGGAGCGGGGCCGCCCTTCCGAGAGGCTCTTCGCCAA
CCTGTGGGGGAGGCTTGAGGGGGAGGAGAGGCTCCTTTGGCTTTACCGGGAGGT
GGAGAGGCCCTTTCCGCTGTCTGGCCACATGGAGGCCACGGGGGTGCGCCT
GGACGTGGCCTATCTCAGGGCCTTGTCCTGGAGGTGGCCGAGGAGATCGCCCG
CCTCGAGGCCGAGGTCTTCCGCCTGGCCGGCCACCCCTTCAACCTCAACTCCCGG
GACCAGCTGGAAAGGGTCTCTTTGACGAGCTAGGGCTTCCCGCCATCGGCAAG
ACGGAGAAGACCGGCAAGCGCTCCACCAGCGCCGCGCTCCTGGAGGCCCTCCGC
GAGGCCACCCCATCGTGGAGAAGATCCTGCAGTACCGGGAGCTCACCAAGCTG
AAGAGCACCTACATTGACCCCTTGCCGGACCTCATCCACCCAGGACGGGGCCGCC
TCCACACCCGCTTCAACCAGACGGCCACGGCCACGGGCAGGCTAAGTAGCTCCG
ATCCCAACCTCCAGA. ACATCCCCGTCCGCACCCCGCTTGGGCAGAGGATCCGCCG
GGCCTTCATCGCCGAGGAGGGGTGGCTATTGGTGGCCCTGGACTATAGCCAGAT
AGAGCTCAGGGTGTGGCCACCTCTCCGGCGACGAGAACCTGATCCGGGTCTTC
CAGGAGGGGGCGGGACATCCACACGGAGACCGCCAGCTGGATGTTCCGGCGTCCCC
CGGGAGGCCGTGGACCCCTGATGCGCCGGGCGGCCAAGACCATCAACTTCGGG
GTCCTCTACGGCATGTGCGGCCACCGCCTCTCCAGGAGCTAGCCATCCCTTACG
AGGAGGCCAGGCCTTCATTGAGCGCTACTTTCAGAGCTTCCCCAAGGTGCGGGC

CTGGATTGAGAAGACCCTGGAGGAGGGCAGGAGGCGGGGGTACGTGGAGACCC
TCTTCGGCCGCGCCGCTACGTGCCAGACCTAGAGGCCCGGGTGAAGAGCGTGC
GGGAGGCGGCCGAGCGCATGGCCTTCAACATGCCCCGTCCAGGGCACCGCCGCCG
ACCTCATGAAGCTGGCTATGGTGAAGCTCTTCCCCAGGCTGGAGGAAATGGGGG
CCAGGATGCTCCTTCAGGTCCACGACGAGCTGGTCCTCGAGGCCCAAAAGAGA
GGGCGGAGGCCGTGGCCCGGCTGGCCAAGGAGGTCATGGAGGGGGTGTATCCCC
TGGCCGTGCCCCTGGAGGTGGAGGTGGGGATAGGGGAGGACTGGCTCTCCGCCA
AGGAGGGCATTGATGGCCGCGGCGGAGGCGGGCATCATCATCATCATTA

SEQ ID NO: 125 The amino acid sequence of Sso7d-Taq fusion protein.

MITNSSATVKFKYKGEEKEVDISKIKKVWRVGKMISFTYDEGGGKTGRGAVSEKDA
PKELLQMLEKQKKGGGVTS GMLPLFEPKGRVLLVDGHHLAYRTFHALKGLTTSRGE
PVQAVYGF AKSLLKALKEDGDAVIVVFD AKAPSRHEAYGGYKAGRAPTPEDFPRQ
LALIKELVDLLGLARLEVP GYEADDVLASLAKKAEKEGYEVRLTADKDLYQLLSDR
IHVLHPEGYLITPAWLWEKYGLR. PDQWADYRALTGDESDNLPGVKGIGEKTARKLL
EEWGSLEALLKNLDRLKPAIREKILAHMDDLKLSWDLAKVRTDLPLEVDFAKRREP
DRERLRAFLERLEFGSLLHEFGLLLESPKALEEAPWPPPEGAFVGVLSRKEPMWADL
LALAAARGGRVHRAPEPYKALRDLKEARGLLAKDLSVLALREGLGLPPGDDPMLLA
YLLDPSNTTPEGVARRYGGEWTEEAGERAAALSERLFANLWGRLEGEERLLWLYREV
ERPLSAVLAHMEATGVRLDVAYLRALSLEVAEEIARLEAEVFRLAGHPFNLNSRDQL
ERVLFDELGLPAIGKTEKTGKRSTSAAVLEALREAHPIVEKILQYRELTKLKSTYIDPL
PDLIHPRTGRLHTRFNQTATATGRLSSSDPNLQNPVRTPLGQIRJRAFI AEEGWLLVA
LDYSQIELRVL AHLSGDENLIRVFQEGRDIHTETASWMFGVPREAVDPLMRRAAKTI
NFGVLYGMSAHRLSQELAIPEYEAQAFIERYFQSFPKVRAWIEKTLEEGRRRGYVETL
FGRRRYVPDLEARVKS VREAAERMAFNMPVQGT AADLMKLAMVKLFPRLEEMGA
RMLLQVHDEL VLEAPKERA EAVARLAKEVM EGVYPLAVPLEVEVGIGEDWLSAKE
GIDGRGGGGHHHHHH

SEQ ID NO: 126 The DNA sequence encoding the Pfu-Sso7d fusion protein

ATGATTTT TAGATGTGGATTACATAACTGAAGAAGGAAAACCTGTTATTAGGCTAT
TCAAAAAAAGAGAACGGAAAATTTAAGATAGAGCATGATAGAACTTTTAGACCAT
ACATTTACGCTCTTCTCAGGGATGATTCAAAGATTGAAGAAGTTAAGAAAATAAC
GGGGGAAAGGCATGGAAAGATTGTGAGAATTGTTGATGTAGAGAAGGTTGAGAA
AAAGTTTCTCGGCAAGCCTATTACCGTGTGGAAACTTTATTTGGAACATCCCCAA
GATGTTCCCACTATTAGAGAAAAAGTTAGAGAACATCCAGCAGTTGTGGACATCT
TCGAATACGATATTCCATTTGCAAAGAGATACCTCATCGACAAAGGCCTAATACC
AATGGAGGGGGAAGAAGAGCTAAAGATTCTTGCCTTCGATATAGAAACCCTCTA
TCACGAAGGAGAAGAGTTTGGAAAAGGCCCAATTATAATGATTAGTTATGCAGA
TGAAAATGAAGCAAAGGTGATTACTTGGAAAAACATAGATCTTCCATACGTTGA
GGTTGTATCAAGCGAGAGAGAGATGATAAAGAGATTTCTCAGGATTATCAGGGA
GAAGGATCCTGACATTATAGTTACTTATAATGGGAGACTCATTCGACTTCCCATAT
TTAGCGAAAAGGGCAGAAAAACTTGGGATTAAATTAACCATTTGGAAGAGATGGA
AGCGAGCCCAAGATGCAGAGAATAGGCGATATGACGGCTGTAGAAGTCAAGGG
AAGAATACATTTGACTTGTATCATGTAATAACAAGGACAATAAATCTCCCAACA
TACACACTAGAGGCTGTATATGAAGCAATTTTGGAAAGCCAAAGGAGAAGGTA
TACGCCGACGAGATAGCAAAAGCCTGGGAAAGTGGAGAGAACCTTGAGAGAGTT
GCCAAATACTCGATGGAAGATGCAAAGGCAACTTATGAACTCGGGAAAGAATTC
CTTCCAATGGAAATTCAGCTTTCAAGATTAGTTGGACAACCTTTATGGGATGTTT
CAAGGTCAAGCACAGGGAACCTTGTAGAGTGGTTCTTACTTAGGAAAGCCTACG
AAAGAAACGAAGTAGCTCCAAACAAGCCAAGTGAAGAGGAGTATCAAAGAAGG
CTCAGGGAGAGCTACACAGGTGGATTTCGTTAAAGAGCCAGAAAAGGGGTTGTGG
GAAAACATAGTATACCTAGATTTTAGAGCCCTATATCCCTCGATTATAATTACCC
ACAATGTTTCTCCCGATACTCTAAATCTTGAGGGATGCAAGAACTATGATATCGC
TCCTCAAGTAGGCCACAAGTTCTGCAAGGACATCCCTGGTTTTATACCAAGTCTC

TTGGGACATTTGTTAGAGGAAAGACAAAAGATTAAGACAAAAATGAAGGAAACT
TTAGCAAATTCTTTCTACGGATATTATGGCTATGCAAAGCAAGATGGTACTGTA
AGGAGTGTGCTGAGAGCGTTACTGCCTGGGGAAGAAAGTACATCGAGTTAGTAT
GGAAGGAGCTCGAAGAAAAGTTTGGATTAAAGTCCTCTACATTGACACTGATG
GTCTCTATGCAACTATCCCAGGAGGAGAAAGTGAGGAAATAAAGAAAAAGGCTC
TAGAATTTGTAAAATACATAAATTCAAAGCTCCCTGGACTGCTAGAGCTTGAATA
TGAAGGGTTTTATAAGAGGGGATTCTTCGTTACGAAGAAGAGGTATGCAGTAAT
AGATGAAGAAGGAAAAGTCATTACTCGTGGTTTAGAGATAGTTAGGAGAGATTG
GAGTGAAATTGCAAAGAAACTCAAGCTAGAGTTTTGGAGACAATACTAAAACA
CGGAGATGTTGAAGAAGCTGTGAGAATAGTAAAAGAAGTAATACAAAAGCTTGC
CAATTATGAAATTCCACCAGAGAAGCTCGCAATATATGAGCAGATAACAAGACC
ATTACATGAGTATAAGGCGATAGGTCCTCACGTAGCTGTTGCAAAGAACTAGCT
GCTAAAGGAGTTAAAATAAAGCCAGGAATGGTAATTGGATACATAGTACTTAGA
GGCGATGGTCCAATTAGCAATAGGGCAATTCTAGCTGAGGAATACGATCCCCAA
AAGCACAAAGTATGACGCAGAATATTACATTGAGAACCAGGTTCTTCCAGCGGTA
CTTAGGATATTGGAGGGGATTTGGATACAGAAAGGAAGACCTCAGATACCAAAG
ACAAGACAAGTCGGCCTAACTTCCTGGCTTAACATTAAAAAATCCGGTACCGGC
GGTGGCGGTGCAACCGTAAAGTTCAAGTACAAAGGCGAAGAAAAAGAGGTAGA
CATCTCCAAGATCAAGAAAGTATGGCGTGTGGGCAAGATGATCTCCTTCACCTAC
GACGAGGGCGGTGGCAAGACCGGCCGTGGTGGGTAAGCGAAAAGGACGCGCC
GAAGGAGCTGCTGCAGATGCTGGAGAAGCAGAAAAAGTGA

SEQ ID NO: 127 The amino acid sequence of the Pfu-Sso7d fusion protein

MILDVDYITEEGKPVIRLFKKENGKFKIEHRTFRPYIYALLRDDSKIEEVKKITGERH
GKIVRIVDVEKVEKKFLGKPITVWKLYLEHPQDVPTIREKVREHPAVVDIFEYDIPFA
KRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGKGPIIMISYADENEAKVITWKNID
LPYVEVVSSEREMIKRFLRIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLTIGRDGS
EPKMQRIGDMTAVEVKGRIHFDLYHVITRTINLPTYTLEAVYEAIFGKPKEKVYADEI
AKAWESGENLERVAKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSSSTGN
LVEWFLLRKAYERNEVAPNKPSEEEYQRRRLRESYTGGFVKEPEKGLWENIVYLDFR
ALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFCKDIPGFIPSLLGHLLEERQKIKTK
MKETQDPIEKILLDYRQKAIKLLANSFYGYGYAKARWYCKECAESVTAWGRKYIE
LVWKELEEKFGFKVLYIDTDGLYATIPGGESEEEKKALEFVKYNSKLPGLLELEYE
GFYKRGGFFVTKKRYAVIDEEGKVITRGLEIVRRDWSEIAKETQARVLETILKHGDVEE
AVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAGVKIKPG
MVIGYTVLRGDGPISNRAILAEYDPKKHKYDAEYYIENQVLPVLRILEGFGYRKED
LRYQKTRQVGLTSWLNKKSGTGGGGATVKFKYKGEEKEVDISKIKKVWRVGMIS
FTYDEGGGKTGRGAVSEKDAPKELLQMLEKQKK

SEQ ID NO: 128 The DNA sequence encoding the Sac7d-ΔTaq fusion protein

atgattacga	attcgacggt	gaaggtaaag	ttcaagtata	agggtgaaga	gaaagaagta
gacacttcaa	agataaagaa	ggtttgagga	gtaggcaaaa	tggtgtcctt	tacctatgac
gacaatggta	agacaggtag	aggagctgta	agcgagaaag	atgctccaaa	agaattatta
gacatgtag	caagagcaga	aagagagaag	aaaggcggcg	gtgtcactag	ccccaaggcc
ctggaggagg	ccccctggcc	cccgccggaa	ggggccttcg	tgggctttgt	gctttcccgc
aaggagccca	tgtgggcccga	tcttctggcc	ctggccggcg	ccaggggggg	ccgggtccac
cgggcccccg	agccttataa	agccctcagg	gacctgaagg	aggcgcgggg	gcttctcgcc
aaagacctga	gcgttctggc	cctgagggaa	ggccttggcc	tcccgcccg	cgacgacccc
atgctcctcg	cctacctcct	ggacccttcc	aacaccaccc	ccgagggggg	ggcccggcgc
tacggcgggg	agtggacgga	ggaggcgggg	gagcggggcg	ccctttccga	gaggctcttc
gccaacctgt	gggggagggt	tgaggggggag	gagaggctcc	tttggttta	ccgggagggtg
gagaggcccc	tttccgctgt	cctggcccac	atggaggcca	cggggggtgcg	cctggacgtg
gcctatctca	gggccttgtc	cctggagggtg	gccgaggaga	tcgcccgcct	cgaggccgag
gtcttcgcgc	tggccggcca	ccccctcaac	ctcaactccc	gggaccagct	ggaaagggtc
ctctttgacg	agctagggtc	tcccgccatc	ggcaagacgg	agaagaccgg	caagcgctcc
accagcgccg	ccgtcctgga	ggccctccgc	gaggccacc	ccatcggtga	gaagatcctg
cagtaccggg	agctcaccaa	gctgaagagc	acctacattg	accccttgcc	ggacctcatc

caccccagga cgggcccgcct ccacaccgc ttcaaccaga cggccacggc cacgggcagg
ctaagtagct ccgatcccaa cctccagaac atccccgtcc gcaccccgtc tgggcagagg
atccgccggg ccttcacgc cgaggagggg tggctattgg tggccctgga ctatagccag
atagagctca ggggtgctggc ccacctctcc ggcgacgaga acctgatccg ggtcttccag
gaggggcggg acatccacac ggagaccgcc agctggatgt tcggcgtccc ccgggaggcc
gtggaccccc tgatgcgcgc ggcggccaag accatcaact tcggggtcct ctacggcatg
tcggcccacc gcctctcca ggagctagcc atcccttacg aggaggcca ggccttcatt
gagcgctact ttcagagctt cccaaggtg cgggcctgga ttgagaagac cctggaggag
ggcaggaggc gggggtacgt ggagaccctc ttcggccgcc gccgctacgt gccagaccta
gagggccggg tgaagagcgt gcgggaggcg gccgagcgca tggccttcaa catgcccgtc
cagggcaccg ccgccgacct catgaagctg gctatggtga agctcttccc caggctggag
gaaatggggg ccaggatgct ccttcaggct cagcagagc tggctctcga ggccccaaa
gagagggcgg aggcgtggc ccggctggcc aaggaggtca tggagggggg gtatcccctg
gccgtgcccc tggaggtgga ggtggggata ggggaggact ggctctccgc caaggagggc
attgatggcc gcggcggagg cgggcatcat catcatcatc attaa

SEQ ID NO: 129 The amino acid sequence of the Sac7d-ΔTaq fusion protein

MITNSTVKVKFKYKGEEKEVDTSKIKKVWRVGKMVSFTYDDNGKTGRGAVSEKDA
PKELLDMLARAEREKKGGGVTS PKALEEAPWPPPEGAFVGVLSRKEPMWADLLAL
AAARGGRVHRAPEPYKALRDLKEARGLLAKDLSVLALREGLGLPPGDDPMLLAYLL
DPSNTTPEGVARRYGGEWTEEAGERAAALSERLFANLWGRLEGEERLLWLYREVERP
LSAVLAHMEATGVRLDVAYLRALSLEVAEELARLEAEVFRLAGHPFNLSRDQLERV
LFDELGLPAIGKTEKTGKRSTSAVLEALREAHPIVEKILQYRELTKLKSTYIDPLPLDI
HPRTGRLHTRFNQTATATGRLSSSDPNLQNPVRTPLGQIRRAFIAEEGWLLVALDY
SQIELRVLAHLSGDENLIRVFQEGRDIHTETASWMFGVPREAVDPLMRRAAKTINFG
VLYGMSAHLRSQELAIPEYEAQAFIERFYQSFPKVRAWIEKTLEEGRRRGYVETLFR
RRYVPDLEARVKSVREAAERMAFNMPVQGTAADLMKLMVKLFPRLEEMGARM
LQVHDELVLEAPKERA EAVARLAKEVMGVYPLAVPLEVEVGIGEDWLSAKEGIDG
RGGGGHHHHHH

SEQ ID NO: 130 The DNA sequence encoding the PL-ΔTaq fusion protein

ATGATTACGAATTCGAAGAAAAAGAAAAAGAAAAAGCGTAAGAAACGCAAAAA
GAAAAAGAAAGGCGGCGGTGTCAGTGGCGCAACCGTAAAGTTCAAGTACAA
AGGCGAAGAAAAAGAGGTAGACATCTCCAAGATCAAGAAAGTATGGCGTGTGG
GCAAGATGATCTCCTTCACCTACGACGAGGGCGGTGGCAAGACCGGCCGTGGTG
CGGTAAGCGAAAAGGACGCGCCGAAGGAGCTGCTGCAGATGCTGGAGAAGCAG
AAAAAGGGCGGCGGTGTCACCAGTCCCAAGGCCCTGGAGGAGGCCCTGGCCC
CCGCCGGAAGGGGCTTCGTGGGCTTTGTGCTTTCCCGCAAGGAGCCCATGTGGG
CCGATCTTCTGGCCCTGGCCGCCGCGCCAGGGGGGGCCGGGTCCACCGGGCCCCCG
AGCCTTATAAAGCCCTCAGGGACCTGAAGGAGGCGCGGGGGCTTCTCGCCAAAG
ACCTGAGCGTTCTGGCCCTGAGGGAAGGCCTTGGCCTCCCGCCCGGCGACGACCC
CATGCTCCTCGCCTACCTCCTGGACCCTTCCAACACCAACCCCGAGGGGGTGGCC
CGGCGCTACGGCGGGGAGTGGACGGAGGAGGCGGGGGAGCGGGCCGCCCTTTCC
GAGAGGCTCTTCGCCAACCTGTGGGGGAGGCTTGAGGGGGAGGAGAGGCTCCTT
TGGCTTTACCGGGAGGTGGAGAGGCCCTTTCCGCTGTCCTGGCCACATGGAGG
CCACGGGGGTGCGCCTGGACGTGGCCTATCTCAGGGCCTTGTCCCTGGAGGTGGC
CGAGGAGATCGCCCGCCTCGAGGCCGAGGTCTTCGCTGGCCGGCCACCCCTTC
AACCTCAACTCCCGGGACCACTGGAAAGGGTCTCTTTGACGAGCTAGGGCTTC
CCGCCATCGGCAAGACGGAGAAGACCGGCAAGCGCTCCACCAGCGCCGCCGTCC
TGGAGGCCCTCCGCGAGGCCCAACCCATCGTGGAGAAGATCCTGCAGTACCGGG
AGCTACCAAGCTGAAGAGCACCTACATTGACCCCTTGCCGGACCTCATCCACCC
CAGGACGGGCGCCTCCACACCCGCTTCAACCAGACGGCCACGGCCACGGGCAG
GCTAAGTAGCTCCGATCCCAACCTCCAGAACATCCCCGTCCGCACCCCGCTTGGG
CAGAGGATCCGCCGGGCTTCATCGCCGAGGAGGGGTGGCTATTGGTGGCCCTG
GACTATAGCCAGATAGAGCTCAGGGTGCTGGCCACCTCTCCGGCGACGAGAAC
CTGATCCGGGTCTTCCAGGAGGGGGCGGGACATCCACACGGAGACCGCCAGCTGG

ATGTTTCGGCGTCCCCCGGGAGGCCGTGGACCCCCTGATGCGCCGGGCGGCCAAG
ACCATCAACTTCGGGGTCTCTACGGCATGTCGGCCCACCGCCTCTCCCAGGAGC
TAGCCATCCCTTACGAGGAGGCCAGGCCTTCATTGAGCGCTACTTTCAGAGCTT
CCCCAAGGTGCGGGCCTGGATTGAGAAGACCCTGGAGGAGGGCAGGAGGCGGG
GGTACGTGGAGACCCTCTTCGGCCGCGCCGCTACGTGCCAGACCTAGAGGCCC
GGGTGAAGAGCGTGCGGGAGGCGGCCGAGCGCATGGCCTTCAACATGCCCCGTCC
AGGGCACCGCCGCCGACCTCATGAAGCTGGCTATGGTGAAGCTCTTCCCCAGGCT
GGAGGAAATGGGGGCCAGGATGCTCCTTCAGGTCCACGACGAGCTGGTCCTCGA
GGCCCCAAAAGAGAGGGCGGAGGCCGTGGCCCGGCTGGCCAAGGAGGTCATGG
AGGGGGTGTATCCCCTGGCCGTGCCCCTGGAGGTGGAGGTGGGGATAGGGGAGG
ACTGGCTCTCCGCCAAGGAGGGCATTGATGGCCGCGGCGGAGGCGGGCATCATC
ATCATCATCATTA

SEQ ID NO: 131 The amino acid sequence of PL- Δ Taq fusion protein

MITNSKKKKKKRKKRKKKKKGGGVTS GATVKFKYKGEEKEVDISKIKKVWRVGK
MISFTYDEGGGKTGRGAVSEKDAPKELLQMLEKQKKGGGVTS PKALEEAPWPPPEG
AFVGFVLSRKEPMWADLLALAAARGGRVHRAPEPYKALRDLKEARGLLAKDLSVL
ALREGLGLPPGDDPMLLAYLLDPSNTTPEGVARRYGGEWTEEAGERAALSERLFAN
LWGRLEGEERLLWLYREVERPLSAVLAHMEATGVRLDVAYLRALSLEVAEEIARLE
AEVFRLAGHPFNLNSRDQLERVLFDELGLPAIGKTEKTGKRSTSAAVLEALREAHPIV
EKILQYRELTKLKSTYIDPLPDLIHPRTGRLHTRFNQTATATGRLSSSDPNLQNIPVRTP
LGQRIRRAFIAEEGWLLVALDYSQIELRVLAHLSGDENLIRVFQEGRDIHTETASWMF
GVPREAVDPLMRRAAKTINFGVLYGMSAHRLSQELAIPEYEEAQAFIERYFQSFPKVR
AWIEKTLEEGRRRGYVETLFGRRRYVPDLEARVKS VREAAERMAFNMPVQGTAAAD
LMKLAMVKLFPRLEEMGARMLLQVHDELVLEAPKERA EAVARLAKEVMEGVYPL
AVPLEVEVGIGEDWLSAKEGIDGRGGGGHHHHHH

SEQ ID NO: 132 PRIMER L71F 5'-CCTGCTCTGCCGCTTCACGC-3'

SEQ ID NO: 133 PRIMER L71R 5'-GCACAGCGGCTGGCTGAGGA-3'

SEQ ID NO: 134 PRIMER L18015F 15 5'-TGACGGAGGATAACGCCAGCAG-3'

SEQ ID NO: 135 PRIMER L23474R 5'-GAAAGACGA TGGGTCGCTAATACGC-3'

SEQ ID NO: 136 PRIMER L18015F 5'-TGACGGAGGATAAC GCCAGCAG-3'

SEQ ID NO: 137 PRIMER L29930R 5'-GGGGTTGGAGGTCAATGGGTTC-3'

SEQ ID NO: 138 PRIMER L30350F 5'-CCTGCTCTGCCGCTTCACGC-3'

SEQ ID NO: 139 PRIMER L3512IR 30 5'-CACATGGTACAGCAAGCCTGGC-3'

SEQ ID NO: 140 PRIMER L2089F 5'-CCCGTATCTGCTGGGA TACTGGC-3'

SEQ ID NO: 141 PRIMER L7112R 5'-CAGCGGTGCTGACTGAATCATGG-3'

SEQ ID NO: 142 PRIMER L30350F 5'-CCTGCCTGCCGCTTCACGC-3'

SEQ ID NO: 143 PRIMER L40547R 5'-CCAATACCCGTTTCA TCGCGGC-3'

SEQ ID NO: 144 PRIMER H-Amelo-Y 5'-CCACCTCATCCTGG GCACC-3'

SEQ ID NO: 145 PRIMER H-Amelo-YR 5'-GCTTGAGGCCAACCATCAGAGC-3'

SEQ ID NO: 146 Human beta-globin primer 536F 5'-GGTTGGCCAATCTACTCCCAGG-3'

SEQ ID NO: 147 Human beta-globin primer 536R 5'-GCTCACTCAGTGTGGCAAAG-3'

SEQ ID NO: 148 Human beta-globin primer 1408R 5'-GATTAGCAAAAGGGCCTAGCTTGG- 3'

Figure 20

PURIFIED THERMOSTABLE PYROCOCCUS FURIOSUS DNA POLYMERASE I

AMINO ACID SEQUENCE (SEQ ID NO: 62)

Met	Ile	Leu	Asp	Val	Asp	Tyr	Ile	Thr	Glu	Glu	Gly	Lys	Pro	Val	Ile	1	5	10	15
Arg	Leu	Phe	Lys	Lys	Glu	Asn	Gly	Lys	Phe	Lys	Ile	Glu	His	Asp	Arg	20	25	30	
Thr	Phe	Arg	Pro	Tyr	Ile	Tyr	Ala	Leu	Leu	Arg	Asp	Asp	Ser	Lys	Ile	35	40	45	
Glu	Glu	Val	Lys	Lys	Ile	Thr	Gly	Glu	Arg	His	Gly	Lys	Ile	Val	Arg	50	55	60	
Ile	Val	Asp	Val	Glu	Lys	Val	Glu	Lys	Lys	Phe	Leu	Gly	Lys	Pro	Ile	65	70	75	80
Thr	Val	Trp	Lys	Leu	Tyr	Leu	Glu	His	Pro	Gln	Asp	Val	Pro	Thr	Ile	85	90	95	
Arg	Glu	Lys	Val	Arg	Glu	His	Pro	Ala	Val	Val	Asp	Ile	Phe	Glu	Tyr	100	105	110	
Asp	Ile	Pro	Phe	Ala	Lys	Arg	Tyr	Leu	Ile	Asp	Lys	Gly	Leu	Ile	Pro	115	120	125	
Met	Glu	Gly	Glu	Glu	Glu	Leu	Lys	Ile	Leu	Ala	Phe	Asp	Ile	Glu	Thr	130	135	140	
Leu	Tyr	His	Glu	Gly	Glu	Glu	Phe	Gly	Lys	Gly	Pro	Ile	Ile	Met	Ile	145	150	155	160
Ser	Tyr	Ala	Asp	Glu	Asn	Glu	Ala	Lys	Val	Ile	Thr	Trp	Lys	Asn	Ile	165	170	175	
Asp	Leu	Pro	Tyr	Val	Glu	Val	Val	Ser	Ser	Glu	Arg	Glu	Met	Ile	Lys	180	185	190	
Arg	Phe	Leu	Arg	Ile	Ile	Arg	Glu	Lys	Asp	Pro	Asp	Ile	Ile	Val	Thr	195	200	205	
Tyr	Asn	Gly	Asp	Ser	Phe	Asp	Phe	Pro	Tyr	Leu	Ala	Lys	Arg	Ala	Glu	210	215	220	
Lys	Leu	Gly	Ile	Lys	Leu	Thr	Ile	Gly	Arg	Asp	Gly	Ser	Glu	Pro	Lys	225	230	235	240
Met	Gln	Arg	Ile	Gly	Asp	Met	Thr	Ala	Val	Glu	Val	Lys	Gly	Arg	Ile	245	250	255	
His	Phe	Asp	Leu	Tyr	His	Val	Ile	Thr	Arg	Thr	Ile	Asn	Leu	Pro	Thr	260	265	270	

Replacement Figure

Glu	Leu	Glu	Tyr	Glu	Gly	Phe	Tyr	Lys	Arg	Gly	Phe	Phe	Val	Thr	Lys			
			580					585					590					
Lys	Arg	Tyr	Ala	Val	Ile	Asp	Glu	Glu	Gly	Lys	Val	Ile	Thr	Arg	Gly			
		595					600					605						
Leu	Glu	Ile	Val	Arg	Arg	Asp	Trp	Ser	Glu	Ile	Ala	Lys	Glu	Thr	Gln			
	610					615					620							
Ala	Arg	Val	Leu	Glu	Thr	Ile	Leu	Lys	His	Gly	Asp	Val	Glu	Glu	Ala			
625					630					635					640			
Val	Arg	Ile	Val	Lys	Glu	Val	Ile	Gln	Lys	Leu	Ala	Asn	Tyr	Glu	Ile			
			645					650						655				
Pro	Pro	Glu	Lys	Leu	Ala	Ile	Tyr	Glu	Gln	Ile	Thr	Arg	Pro	Leu	His			
		660						665					670					
Glu	Tyr	Lys	Ala	Ile	Gly	Pro	His	Val	Ala	Val	Ala	Lys	Lys	Leu	Ala			
	675						680					685						
Ala	Lys	Gly	Val	Lys	Ile	Lys	Pro	Gly	Met	Val	Ile	Gly	Tyr	Ile	Val			
	690					695					700							
Leu	Arg	Gly	Asp	Gly	Pro	Ile	Ser	Asn	Arg	Ala	Ile	Leu	Ala	Glu	Glu			
705					710					715					720			
Tyr	Asp	Pro	Lys	Lys	His	Lys	Tyr	Asp	Ala	Glu	Tyr	Tyr	Ile	Glu	Asn			
			725						730					735				
Gln	Val	Leu	Pro	Ala	Val	Leu	Arg	Ile	Leu	Glu	Gly	Phe	Gly	Tyr	Arg			
		740						745					750					
Lys	Glu	Asp	Leu	Arg	Tyr	Gln	Lys	Thr	Arg	Gln	Val	Gly	Leu	Thr	Ser			
	755						760					765						
Trp	Leu	Asn	Ile	Lys	Lys	Ser												
	770				775													

PURIFIED THERMOSTABLE PYROCOCCUS FURIOSUS DNA POLYMERASE I

NUCLEOTIDE SEQUENCE (SEQ ID NO: 61)

ccctggtcct	gggtccacat	atatgttctt	actcgccttt	atgaagaatc	ccccagtcgc	60
tctaacctgg	gttatagtga	caaatcttcc	tccaccaccg	ccaagaagg	ttatttctat	120
caactctaca	cctcccctat	tttctctctt	atgagatttt	taagtatagt	tatagagaag	180
gttttatact	ccaaactgag	ttagtagata	tgtggggagc	ataatgattt	tagatgtgga	240
ttacataact	gaagaaggaa	aacctgttat	taggctattc	aaaaaagaga	acggaaaatt	300
taagatagag	catgatagaa	cttttagacc	atacatttac	gctcttctca	gggatgattc	360
aaagattgaa	gaagttaaga	aaataacggg	ggaaaggcat	ggaaagattg	tgagaattgt	420

Replacement Figure

tgatgtagag aaggttgaga aaaagtttct cggcaagcct attaccgtgt ggaaacttta	480
tttggaaacat cccaagatg ttcccactat tagagaaaaa gttagagaac atccagcagt	540
tgtggacatc ttcgaatacg atattccatt tgcaaagaga tacctcatcg acaaaggcct	600
aataccaatg gagggggaag aagagctaaa gattcttgcc ttcgatatag aaaccctcta	660
tcacgaagga gaagagtttg gaaaaggccc aattataatg attagttatg cagatgaaaa	720
tgaagcaaag gtgattactt ggaaaaacat agatcttcca tacgttgagg ttgtatcaag	780
cgagagagag atgataaaga gatttctcag gattatcagg gagaaggatc ctgacattat	840
agttacttat aatggagact cattcgactt cccatattta gcgaaaaggg cagaaaaact	900
tgggattaaa ttaaccattg gaagagatgg aagcgagccc aagatgcaga gaataggcga	960
tatgacggct gtagaagtca agggaagaat acatttcgac ttgtatcatg taataacaag	1020
gacaataaat ctccaacat acacactaga ggctgtatat gaagcaattt ttggaaagcc	1080
aaaggagaag gtatacgccg acgagatagc aaaagcctgg gaaagtggag agaaccttga	1140
gagagttgcc aaatactcga tggaagatgc aaaggcaact tatgaactcg ggaaagaatt	1200
ccttccaatg gaaattcagc tttcaagatt agttggacaa cctttatggg atgtttcaag	1260
gtcaagcaca gggaaccttg tagagtggtt cttacttagg aaagcctacg aaagaaacga	1320
agtagctcca aacaagccaa gtgaagagga gtatcaaaga aggctcaggg agagctacac	1380
aggtggattc gttaaagagc cagaaaaggg gttgtgggaa aacatagtat acctagattt	1440
tagagcccta tatccctcga ttataattac ccacaatgtt tctcccgata ctctaaatct	1500
tgagggatgc aagaactatg atatcgctcc tcaagtaggc cacaagttct gcaaggacat	1560
ccctggtttt ataccaagtc tcttgggaca tttgttagag gaaagacaaa agattaagac	1620
aaaaatgaag gaaactcaag atcctataga aaaaatactc cttgactata gacaaaaagc	1680
gataaaaactc ttagcaaatt ctttctacgg atattatggc tatgcaaaag caagatggta	1740
ctgtaaggag tgtgctgaga gcgttactgc ctggggaaga aagtacatcg agttagtatg	1800
gaaggagctc gaagaaaagt ttggatttaa agtcctctac attgacactg atggtctcta	1860
tgcaactatc ccaggaggag aaagtgagga aataaagaaa aaggctctag aatttgtaaa	1920
atacataaat tcaaagctcc ctggactgct agagcttgaa tatgaagggt ttataagag	1980
gggattcttc gttacgaaga agaggtatgc agtaatagat gaagaaggaa aagtcattac	2040
tcgtggttta gagatagtta ggagagattg gagtgaatt gcaaaagaaa ctcaagctag	2100
agttttggag acaatactaa aacacggaga tgttgaagaa gctgtgagaa tagtaaaaga	2160

Replacement Figure

agtaatacaa aagcttgcca attatgaaat tccaccagag aagctcgcaa tatatgagca	2220
gataacaaga ccattacatg agtataaggc gataggtcct cacgtagctg ttgcaaagaa	2280
actagctgct aaaggagtta aaataaagcc aggaatggta attggataca tagtacttag	2340
aggcgatggc ccaattagca atagggcaat tctagctgag gaatacgatc ccaaaaagca	2400
caagtatgac gcagaatatt acattgagaa ccaggttctt ccagcggtag ttaggatatt	2460
ggagggattt ggatacagaa aggaagacct cagataccaa aagacaagac aagtcggcct	2520
aacttcctgg cttaacatta aaaaatccta gaaaagcgat agatatcaac ttttattctt	2580
tctaaccctt ttctatgaaa gaagaactga gcaggaatta ccagttcttc cgttatttta	2640
tgggtaatta aaaacccatg ctcttgggag aatcttcgaa taaaatccct aacttcaggc	2700
tttgctaagt gaatagaata aacaacatca ctcaactcaa acgccttcgt tagaaatggc	2760
ctatctgcat gcttctctgg ctcggaanng gaggattcat aacaacagta tcaacattct	2820
cagagaattg agaaacatca gaaactttga cttctacaac atttctaact ttgcaactct	2880
tcaagatttt ctaaaagaat tttaacggcc tcctcgtcaa tttcgacgac gtagatcttt	2940
tttgctccaa gcagagccgc tccaatggat aacaccctg ttcccgacc caagtccgct	3000
acaatttttt ccttgatatct cctaattgat aagcaagcca aaggagagta gatgctacct	3060
ttccgggagt tttgtattgc tctagccaag gtttgggatt tttgaatcct ttaactctgg	3120
aaagtataat ttcaagctcc ttcttcttca tgacagatga aaaattgttt tgtctctttt	3180
taactttttac agaaataact gtctcaaatt atgacaactc ttgacatttt tacttcatta	3240
ccagggtaat gtttttaagt atgaaatttt tctttcatag aggaggnnnn nngtcctctc	3300
ctcgatttcc ttggttgtgc tccatatgat aagcttccaa agtgggtgtt cagactttta	3360
gacactcaaa taccagacga caatgggtgtg ctcaactcaag ccccatatgg gttgagaaaa	3420
gtagaagcgg cactactcag atgcttcccc aggaatgagg ttgttgtagc tcntcccnga	3480
aagattgaga tggttcttgg	3499